



## results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057859611-03868-12851

Query= SEQID28  
(9 letters)

**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,477,204 sequences; 474,244,320 total letters

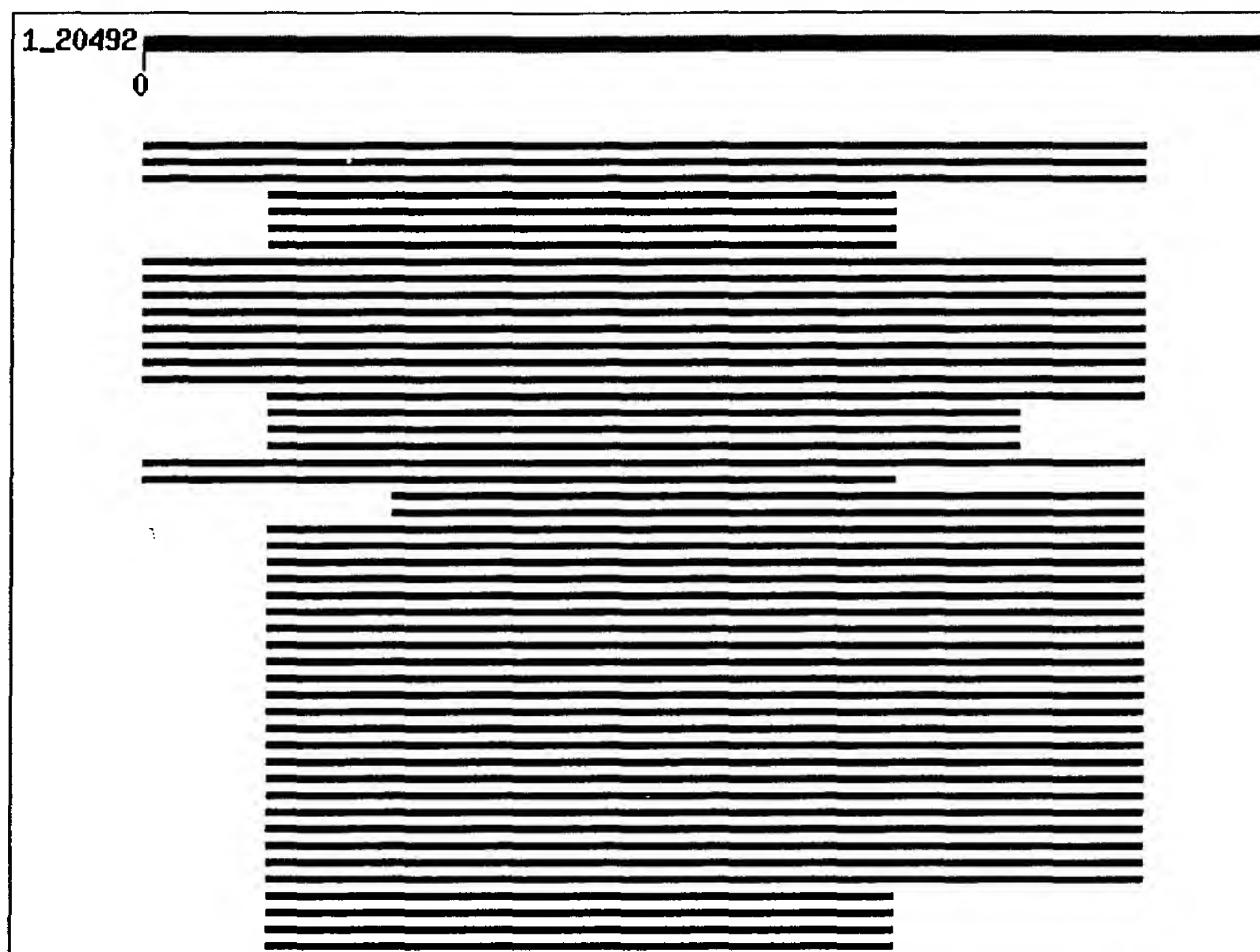
If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

### Distribution of 128 Blast Hits on the Query Sequence

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Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

	Score (bits)	E Value	
gi 21355617 ref NP_651115.1  CG10873-PA [Drosophila melanog...	34	0.22	L
gi 25009887 gb AAN71112.1  AT28346p [Drosophila melanogaster]	34	0.22	
gi 31207283 ref XP_312608.1  ENSANGP00000014785 [Anopheles ...	31	1.8	
gi 1709335 sp P21783 NOTC_XENLA Neurogenic locus notch prot...	24	194	
gi 18859115 ref NP_571516.1  notch homolog 1a; neurogenic 1...	24	194	L
gi 27675874 ref XP_228125.1  similar to 40kDa ribosomal pro...	24	194	L
gi 104252 pir A35844 Xotch protein - African clawed frog	24	194	
gi 9626079 ref NP_040318.1  Non-capsid protein [Parvovirus ...	23	468	
gi 22966887 ref ZP_00014482.1  hypothetical protein [Rhodos...	23	468	
gi 22137819 gb AAM93277.1 AF332883_1 nonstructural protein ...	23	468	
gi 8928081 sp Q9ZA11 DHAL_RHORU Aldehyde dehydrogenase >gi ...	23	468	
gi 21238945 dbj BAB96577.1  aldehyde dehydrogenase [Cytopha...	23	468	
gi 23113187 ref ZP_00098587.1  hypothetical protein [Desulf...	23	468	
gi 22137816 gb AAM93275.1 AF332882_1 nonstructural protein ...	23	468	
gi 3033510 gb AAC40695.1  nonstructural protein [Kilham rat...	23	468	
gi 1711120 gb AAB38326.1  non-capsid protein [Kilham rat vi...	23	468	
gi 22137811 gb AAM93272.1 AF321230_1 nonstructural protein ...	23	468	
gi 22137822 gb AAM93279.1 AF332884_1 nonstructural protein ...	23	468	
gi 29823071 ref NP_821154.1  Nonstructural protein NS1 [LuI...	23	468	
gi 18150104 dbj BAB83667.1  insulin receptor [Paralichthys ...	22	843	
gi 31205321 ref XP_311609.1  ENSANGP00000016117 [Anopheles ...	22	843	
gi 23867780 dbj BAC21014.1  claudin4L2 [Xenopus laevis]	22	843	
gi 12848262 dbj BAB27889.1  unnamed protein product [Mus mu...	22	843	L
gi 3695096 gb AAC62642.1  DN p63 gamma [Mus musculus]	22	1131	L
gi 13751181 emb CAC37102.1  DN KET gamma protein [Rattus no...	22	1131	L

gi 13751173 emb CAC37098.1	TA1 KET alpha protein [Rattus n...	22	1131	L
gi 13626617 sp Q9TV36 FBN1_PIG	Fibrillin 1 precursor >gi 57...	22	1131	
gi 3688648 gb AAC62317.1	mutant fibrillin-1 [Mus musculus]	22	1131	L
gi 20428532 gb AAK81886.1	DN p73 gamma [Homo sapiens]	22	1131	L
gi 1813455 gb AAB41833.1	p53	22	1131	
gi 19909983 dbj BAB87245.1	deltaN p73 beta [Homo sapiens] ...	22	1131	L
gi 7248451 gb AAF43492.1	p51 isoform delNbeta [Homo sapiens]	22	1131	
gi 642072 gb AAA61825.1	fibrillin-1	22	1131	L
gi 13929178 ref NP_114013.1	fibrillin-1 [Rattus norvegicus...	22	1131	L
gi 20892181 ref XP_147232.1	transformation related protein...	22	1131	L
gi 3695094 gb AAC62641.1	TA*p63 alpha [Mus musculus]	22	1131	L
gi 12060406 dbj BAB20591.1	delta N p73L [Homo sapiens]	22	1131	
gi 4803651 emb CAA72225.1	P73 splice variant [Cercopithec...	22	1131	
gi 13751179 emb CAC37101.1	TA2 KET gamma protein [Rattus n...	22	1131	L
gi 15072750 emb CAC48053.1	p63 delta [Homo sapiens]	22	1131	
gi 29470179 gb AAO74632.1	p73 [Danio rerio]	22	1131	
gi 2581764 gb AAB82420.1	p53 [Cricetulus griseus]	22	1131	
gi 24430141 ref NP_000129.2	fibrillin 1 [Homo sapiens]	22	1131	L
gi 8217484 emb CAB92742.1	dJ1092A11.2 (tumor protein p73) ...	22	1131	
gi 2370178 emb CAA72221.1	second splice variant [Homo sapi...	22	1131	L
gi 15678984 ref NP_276101.1	conserved protein [Methanother...	22	1131	
gi 21264484 sp P79820 P53_ORYLA	Cellular tumor antigen p53 ...	22	1131	
gi 1184759 gb AAA87577.1	p53 tumor suppressor homolog	22	1131	
gi 1184757 gb AAA87576.1	p53 tumor suppressor homolog	22	1131	
gi 7248450 gb AAF43491.1	p51 isoform delNalpha [Homo sapiens]	22	1131	
gi 7459676 pir A47221	fibrillin 1 precursor - human (fragm...	22	1131	
gi 7248447 gb AAF43488.1	p51 isoform TAp63beta [Homo sapiens]	22	1131	
gi 3273745 gb AAC24830.1	p53 homolog [Homo sapiens]	22	1131	L
gi 473579 gb AAB41344.1	tumor supressor p53 [Mesocricetus ...]	22	1131	
gi 27527178 emb CAD10682.1	p53 protein [Monodelphis domest...	22	1131	
gi 12024746 gb AAG45609.1	TA p63 gamma [Homo sapiens]	22	1131	
gi 3695098 gb AAC62643.1	DN p63 beta [Mus musculus]	22	1131	L
gi 4689086 gb AAD27752.1 AF043641_1	p73 [Barbus barbus]	22	1131	
gi 6755883 ref NP_035771.1	transformation related protein ...	22	1131	L
gi 1244762 gb AAA98563.1	p53 tumor suppressor homolog	22	1131	
gi 13751187 emb CAC37105.1	DN KET beta protein [Rattus nor...	22	1131	L
gi 13751175 emb CAC37099.1	DN KET alpha protein [Rattus no...	22	1131	L
gi 17554334 ref NP_498645.1	MUscle Positioning 4, transmem...	22	1131	L
gi 23308709 ref NP_694518.1	deltaNp63 isoform alpha 1; tum...	22	1131	L
gi 26339452 dbj BAC33397.1	unnamed protein product [Mus mu...	22	1131	
gi 23308711 ref NP_694519.1	deltaNp63 isoform gamma; tumor...	22	1131	L
gi 3695082 gb AAC62635.1	TA p63 alpha [Homo sapiens]	22	1131	L
gi 1698502 gb AAC60146.1	p53 [Oryzias latipes] >gi 1208249...	22	1131	
gi 20850793 ref XP_131858.1	transformation related protein...	22	1131	L
gi 13195250 gb AAK15622.1 AF314148_1	p63 DNA binding protei...	22	1131	
gi 14579227 gb AAK69172.1 AF289202_1	transmembrane matrix r...	22	1131	L
gi 3510328 dbj BAA32592.1	p51A [Homo sapiens] >gi 3695078 ...	22	1131	L
gi 13751185 emb CAC37104.1	TA1 KET beta protein [Rattus no...	22	1131	L
gi 451931 gb AAA37086.1	tumor supressor protein [Mesocrice...	22	1131	
gi 1813453 gb AAB41832.1	p53	22	1131	
gi 2494284 sp Q61554 FBN1_MOUSE	Fibrillin 1 precursor >gi 1...	22	1131	L

gi 3695080 gb AAC62634.1	DN p63 gamma [Homo sapiens]	>gi 7...	22	1131	<b>L</b>
gi 1813451 gb AAB41831.1	p53		22	1131	
gi 25395876 pir F88508	protein H14A12.6 [imported] - Caeno...		22	1131	
gi 3970717 emb CAA76562.1	KET protein [Homo sapiens]		22	1131	<b>L</b>
gi 23308685 ref NP_689454.1	deltaNp63 isoform alpha 2; tum...		22	1131	<b>L</b>
gi 3445484 dbj BAA32433.1	p73H [Homo sapiens]		22	1131	<b>L</b>
gi 7689271 gb AAF67733.1 AF253323_1	p53 tumor suppressor-li...		22	1131	
gi 6679759 ref NP_032019.1	fibrillin 1; tight skin [Mus mu...		22	1131	<b>L</b>
gi 17985367 gb AAL50211.1	tumor protein [Canis familiaris]		22	1131	
gi 31543818 ref NP_003713.3	tumor protein p73-like; tumor ...		22	1131	<b>L</b>
gi 19909981 dbj BAB87244.1	deltaN p73 alpha [Homo sapiens]...		22	1131	<b>L</b>
gi 4101546 gb AAD01196.1	tumor suppressor protein p53 [Ory...		22	1131	
gi 1813457 gb AAB41834.1	p53		22	1131	
gi 1244764 gb AAA98564.1	p53 tumor suppressor homolog		22	1131	
gi 7440008 pir JC6176	tumor suppressor protein p53 - Chine...		22	1131	
gi 12856636 dbj BAB30732.1	unnamed protein product [Mus mu...		22	1131	<b>L</b>
gi 19850152 gb AAL99584.1 AF285104_1	p53-like transcription...		22	1131	
gi 7320915 emb CAB81954.1	P73 delta-N protein [Mus musculus]		22	1131	<b>L</b>
gi 129370 sp Q00366 P53_MESAU	Cellular tumor antigen p53 (T...		22	1131	
gi 7689273 gb AAF67734.1 AF253324_1	p73-like protein [Mya a...		22	1131	
gi 3695088 gb AAC62638.1	DN p63 beta [Homo sapiens]	>gi 12...	22	1131	<b>L</b>
gi 27806637 ref NP_776478.1	fibrillin 1 [Bos taurus]	>gi 1...	22	1131	<b>L</b>
gi 2370177 emb CAA72219.1	first splice variant [Homo sapiens]		22	1131	<b>L</b>
gi 28487571 ref XP_192917.2	fibrillin 1 [Mus musculus]		22	1131	<b>L</b>

#### Alignments

☐ >gi|21355617|ref|NP\_651115.1| **L** CG10873-PA [Drosophila melanogaster]  
 gi|7211767|gb|AAF40427.1|AF224713\_1 **L** transcription factor p53 [Drosophila melano  
 gi|7211769|gb|AAF40428.1|AF224714\_1 **L** transcription factor p53 [Drosophila melano  
 gi|7381624|gb|AAF61572.1|AF244918\_1 **L** p53 tumor suppressor-like protein [Drosophi  
 gi|8272608|gb|AAF74277.1|AF250918\_1 **L** transcription factor [Drosophila melanogast  
 gi|8453176|gb|AAF75270.1|AF263722\_1 **L** transcription factor p53 [Drosophila melano  
 gi|10726710|gb|AAF56087.2| **L** CG10873-PA [Drosophila melanogaster]  
 gi|17861528|gb|AAL39241.1| **L** GH11591p [Drosophila melanogaster]  
 gi|18032162|gb|AAL56639.1|AF192555\_1 p53-like regulator of apoptosis and cell cyc  
 melanogaster]  
 Length = 385

Score = 34.1 bits (73), Expect = 0.22  
 Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 KICTCPKRD 9  
           KICTCPKRD  
 Sbjct: 259 KICTCPKRD 267



┌>gi|25009887|gb|AAN71112.1| AT28346p [Drosophila melanogaster]  
Length = 519

Score = 34.1 bits (73), Expect = 0.22  
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 KICTCPKRD 9  
KICTCPKRD  
Sbjct: 393 KICTCPKRD 401

┌>gi|31207283|ref|XP\_312608.1| ENSANGP00000014785 [Anopheles gambiae]  
gi|21295812|gb|EAA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PEST]  
Length = 338

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KICTCPKRD 9  
KIC+CPKRD  
Sbjct: 309 KICSCPARD 317

┌>gi|1709335|sp|P21783|NOTC\_XENLA Neurogenic locus notch protein homolog precursor  
gi|1364263|gb|AAB02039.1| Xotch protein  
Length = 2524

Score = 24.4 bits (50), Expect = 194  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
ICTCPK  
Sbjct: 625 ICTCPK 630

Score = 21.4 bits (43), Expect = 1518  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICTCP 6  
ICTCP  
Sbjct: 396 ICTCP 400

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 1044 CTCP 1047

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 2 ICTC 5  
ICTC  
Sbjct: 775 ICTC 778

┌>gi|18859115|ref|NP\_571516.1| **L** notch homolog 1a; neurogenic locus notch homolog  
rerio]  
gi|1171748|sp|P46530|NTC1\_BRARE Neurogenic locus notch homolog protein 1 precursor  
gi|630926|pir|S42612 transmembrane protein precursor - zebra fish  
gi|433867|emb|CAA48831.1| **L** transmembrane protein-precursor [Danio rerio]  
Length = 2437

Score = 24.4 bits (50), Expect = 194  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
ICTCPK  
Sbjct: 624 ICTCPK 629

Score = 21.4 bits (43), Expect = 1518  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICTCP 6  
ICTCP  
Sbjct: 396 ICTCP 400

Score = 21.4 bits (43), Expect = 1518  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICTCP 6  
ICTCP  
Sbjct: 162 ICTCP 166

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 1043 CTCP 1046

┌>gi|27675874|ref|XP\_228125.1| **L** similar to 40kDa ribosomal protein [Rattus norvegicus]  
Length = 310

Score = 24.4 bits (50), Expect = 194  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
ICTCPK  
Sbjct: 188 ICTCPK 193

>gi|104252|pir|A35844 Xotch protein - African clawed frog  
Length = 2524

Score = 24.4 bits (50), Expect = 194  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
ICTCPK  
Sbjct: 626 ICTCPK 631

Score = 21.4 bits (43), Expect = 1518  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICTCP 6  
ICTCP  
Sbjct: 397 ICTCP 401

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 1045 CTCP 1048

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 2 ICTC 5  
ICTC  
Sbjct: 776 ICTC 779

>gi|9626079|ref|NP\_040318.1| Non-capsid protein [Parvovirus H1]  
gi|138882|sp|P03133|VNCS\_PAVHH NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1)  
gi|73528|pir|UYPVV1 noncapsid protein NS1 - parvovirus H1  
gi|60994|emb|CAA25689.1| Non-capsid protein [Parvovirus H1]  
Length = 672

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
KICT P RD  
Sbjct: 216 KICTSPPRD 224

>gi|22966887|ref|ZP\_00014482.1| hypothetical protein [Rhodospirillum rubrum]  
Length = 337

Score = 23.1 bits (47), Expect = 468  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICTCPKR 8  
ICTCP R  
Sbjct: 131 ICTCPSR 137

>gi|22137819|gb|AAM93277.1|AF332883\_1 nonstructural protein 1 [rat minute virus]  
Length = 672

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
KICT P RD  
Sbjct: 216 KICTSPPRD 224

>gi|8928081|sp|Q9ZA11|DHAL\_RHORU Aldehyde dehydrogenase  
gi|4579692|dbj|BAA75070.1| aldehyde dehydrogenase [Rhodospirillum rubrum]  
Length = 506

Score = 23.1 bits (47), Expect = 468  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICTCPKR 8  
ICTCP R  
Sbjct: 300 ICTCPSR 306

>gi|21238945|dbj|BAB96577.1| aldehyde dehydrogenase [Cytophaga sp. KUC-1]  
Length = 501

Score = 23.1 bits (47), Expect = 468  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICTCPKR 8  
ICTCP R  
Sbjct: 295 ICTCPSR 301

>gi|23113187|ref|ZP\_00098587.1| hypothetical protein [Desulfitobacterium hafnien-  
Length = 590

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 1/9 (11%)

Query: 2 ICT-CPKRD 9  
IC CPKRD  
Sbjct: 78 ICNNCPKRD 86

┌>gi|22137816|gb|AAM93275.1|AF332882\_1 nonstructural protein 1 [rat minute virus  
Length = 672

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
KICT P RD  
Sbjct: 216 KICTSPPRD 224

┌>gi|3033510|gb|AAC40695.1| nonstructural protein [Kilham rat virus]  
Length = 665

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
KICT P RD  
Sbjct: 209 KICTSPPRD 217

┌>gi|1711120|gb|AAB38326.1| non-capsid protein [Kilham rat virus]  
Length = 672

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
KICT P RD  
Sbjct: 216 KICTSPPRD 224

┌>gi|22137811|gb|AAM93272.1|AF321230\_1 nonstructural protein 1 [Kilham rat virus]  
Length = 672

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
KICT P RD  
Sbjct: 216 KICTSPPRD 224

┌>gi|22137822|gb|AAM93279.1|AF332884\_1 nonstructural protein 1 [rat minute virus  
Length = 672

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
KICT P RD  
Sbjct: 216 KICTSPPRD 224



┌>gi|29823071|ref|NP\_821154.1| Nonstructural protein NS1 [LuIII virus]  
gi|549392|sp|P36311|VNCS\_PAVL3 NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1)  
gi|476350|pir||A44276 noncapsid protein NS1 - parvovirus LuIII  
Length = 668

Score = 23.1 bits (47), Expect = 468  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
KICT P RD  
Sbjct: 216 KICTSPPRD 224

┌>gi|18150104|dbj|BAB83667.1| insulin receptor [Paralichthys olivaceus]  
Length = 1369

Score = 22.3 bits (45), Expect = 843  
Identities = 6/9 (66%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9  
K+C CPK D  
Sbjct: 705 KVCACPKTD 713

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 2 ICTC 5  
ICTC  
Sbjct: 17 ICTC 20

┌>gi|31205321|ref|XP\_311609.1| ENSANGP00000016117 [Anopheles gambiae]  
gi|30177715|gb|EAA07139.2| ENSANGP00000016117 [Anopheles gambiae str. PEST]  
Length = 261

Score = 22.3 bits (45), Expect = 843  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KICTCPK 7  
KICTC K  
Sbjct: 223 KICTCTK 229

┌>gi|23867780|dbj|BAC21014.1| claudin4L2 [Xenopus laevis]  
Length = 213

Score = 22.3 bits (45), Expect = 843  
Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 3 CTCPKRD 9  
C+CPKR+  
Sbjct: 183 CSCPKRE 189

┌>gi|12848262|dbj|BAB27889.1| ┐ unnamed protein product [Mus musculus]  
Length = 301

Score = 22.3 bits (45), Expect = 843  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 3 CTCPKRD 9  
CTCP RD  
Sbjct: 16 CTCPPRD 22

┌>gi|3695096|gb|AAC62642.1| ┐ DN p63 gamma [Mus musculus]  
Length = 389

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 250 ICACPGRD 257

┌>gi|13751181|emb|CAC37102.1| ┐ DN KET gamma protein [Rattus norvegicus]  
Length = 393

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 250 ICACPGRD 257

┌>gi|13751173|emb|CAC37098.1| ┐ TA1 KET alpha protein [Rattus norvegicus]  
Length = 663

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 327 ICACPGRD 334

┌>gi|13626617|sp|Q9TV36|FBN1\_PIG Fibrillin 1 precursor  
gi|5739075|gb|AAD50328.1|AF073800\_1 fibrillin-1 precursor [Sus scrofa]  
Length = 2871

Score = 21.8 bits (44), Expect = 1131  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
+CTCPK  
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 100 CTCP 103

 >gi|3688648|gb|AAC62317.1|  mutant fibrillin-1 [Mus musculus]  
Length = 3857

Score = 21.8 bits (44), Expect = 1131  
Identities = 5/6 (83%), Positives = 6/6 (100%)



Query: 2 ICTCPK 7  
+CTCPK  
Sbjct: 1775 VCTCPK 1780

Score = 21.8 bits (44), Expect = 1131  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
+CTCPK  
Sbjct: 791 VCTCPK 796


Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 100 CTCP 103

 >gi|20428532|gb|AAK81886.1|  DN p73 gamma [Homo sapiens]  
Length = 426

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 245 ICACPGRD 252

 >gi|1813455|gb|AAB41833.1| p53  
Length = 238

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 167 ICACPGRD 174

┌>gi|19909983|dbj|BAB87245.1| **L** deltaN p73 beta [Homo sapiens]  
gi|20428530|gb|AAK81885.1| **L** DN p73 beta [Homo sapiens]  
Length = 450

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 245 ICACPGRD 252

┌>gi|7248451|gb|AAF43492.1| p51 isoform delNbeta [Homo sapiens]  
Length = 461

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 250 ICACPGRD 257

┌>gi|642072|gb|AAA61825.1| **L** fibrillin-1  
Length = 1095

Score = 21.8 bits (44), Expect = 1131  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
+CTCPK  
Sbjct: 766 VCTCPK 771

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 75 CTCP 78

┌>gi|13929178|ref|NP\_114013.1| **L** fibrillin-1 [Rattus norvegicus]  
gi|4959650|gb|AAD34438.1| **L** fibrillin-1 [Rattus norvegicus]

Length = 2872

Score = 21.8 bits (44), Expect = 1131  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
+CTCPK  
Sbjct: 790 VCTCPK 795

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 100 CTCP 103

>gi|20892181|ref|XP\_147232.1| **L** transformation related protein 63 [Mus musculus]  
Length = 465

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 129 ICACPGRD 136

>gi|3695094|gb|AAC62641.1| **L** TA\*p63 alpha [Mus musculus]  
Length = 680

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 344 ICACPGRD 351

>gi|12060406|dbj|BAB20591.1| delta N p73L [Homo sapiens]  
Length = 501

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 165 ICACPGRD 172

>gi|4803651|emb|CAA72225.1| P73 splice variant [Cercopithecus aethiops]  
Length = 499



Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 294 ICACPGRD 301

>gi|13751179|emb|CAC37101.1| **L** TA2 KET gamma protein [Rattus norvegicus]  
Length = 487

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 344 ICACPGRD 351

>gi|15072750|emb|CAC48053.1| p63 delta [Homo sapiens]  
Length = 232

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 192 ICACPGRD 199

>gi|29470179|gb|AA074632.1| p73 [Danio rerio]  
Length = 640

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 301 ICACPGRD 308

>gi|2581764|gb|AAB82420.1| p53 [Cricetulus griseus]  
Length = 205

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 149 ICACPGRD 156

>gi|24430141|ref|NP\_000129.2| **L** fibrillin 1 [Homo sapiens]


Length = 2871

Score = 21.8 bits (44), Expect = 1131  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7  
+CTCPK  
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 100 CTCP 103

 >gi|8217484|emb|CAB92742.1| dJ1092A11.2 (tumor protein p73) [Homo sapiens]  
Length = 661


Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 319 ICACPGRD 326

 >gi|2370178|emb|CAA72221.1|  second splice variant [Homo sapiens]  
Length = 588

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 246 ICACPGRD 253

 >gi|15678984|ref|NP\_276101.1| conserved protein [Methanothermobacter thermautotrophicus]  
gi|7446472|pir|C69229 conserved hypothetical protein MTH966 - Methanobacterium  
thermoautotrophicum (strain Delta H)  
gi|2622064|gb|AAB85462.1| conserved protein [Methanothermobacter thermautotrophicus]  
Delta H]  
Length = 444

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICTCPKR 8  
ICTC KR  
Sbjct: 355 ICTCGKR 361

☐ >gi|21264484|sp|P79820|P53\_ORYLA Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|4101544|gb|AAD01195.1| tumor suppressor protein p53 [Oryzias latipes]  
Length = 352

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 255 ICACPGRD 262

☐ >gi|1184759|gb|AAA87577.1| p53 tumor suppressor homolog  
Length = 189

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 90 ICACPGRD 97

☐ >gi|1184757|gb|AAA87576.1| p53 tumor suppressor homolog  
Length = 228

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 98 ICACPGRD 105

☐ >gi|7248450|gb|AAF43491.1| p51 isoform delNalpha [Homo sapiens]  
Length = 586

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9  
IC CP RD  
Sbjct: 250 ICACPGRD 257

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
Posted date: Jul 10, 2003 1:49 AM

Number of letters in database: 474,244,320  
Number of sequences in database: 1,477,204

Lambda	K	H
0.357	0.293	2.11

## Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Hits to DB: 7,800,424

Number of Sequences: 1477204

Number of extensions: 35432

Number of successful extensions: 2351

Number of sequences better than 20000.0: 100

Number of HSP's better than 20000.0 without gapping: 2143

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2351

length of query: 9

length of database: 474,244,320

effective HSP length: 0

effective length of query: 9

effective length of database: 474,244,320

effective search space: 4268198880

effective search space used: 4268198880

T: 11

A: 40

X1: 14 ( 7.2 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 35 (19.8 bits)

S2: 35 (18.0 bits)

## Clustal-W Alignment

CLUSTAL W (1.82) multiple sequence alignment

```
gi|21355617|ref|NP_651115.1|-----MYISQPMSTWHKES-----
gi|25009887|gb|AAN71112.1|WSTEDSCGHKSQLLNKIYLFECTAMSLHKSASFSLTFNQNTSIVSRNSNR
                               :: . . ** ** .:

gi|21355617|ref|NP_651115.1|-----
gi|25009887|gb|AAN71112.1|TIFEAFKEFLDFWDIGNEVSAESAVRVSSNGAFNLPQSFGNESNEYAHLA

gi|21355617|ref|NP_651115.1|-----TDS
gi|25009887|gb|AAN71112.1|TPVDPAYGGNNTNNMMQFTNNLEILANNNSDGNNKINACNKFVCHKGTDS
                               ***

gi|21355617|ref|NP_651115.1|EDDSTEVDIKEDI PKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLR
gi|25009887|gb|AAN71112.1|EDDSTEVDIKEDI PKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLR
                               *****

gi|21355617|ref|NP_651115.1|EMMLQDIQIQANTLPKLENHNIGGYCFSMVLDEPPKSLWMYSIPLNKLYI
gi|25009887|gb|AAN71112.1|EMMLQDIQIQANTLPKLENHNIGGYCFSMVLDEPPKSLWMYSIPLNKLYI
                               *****

gi|21355617|ref|NP_651115.1|RMNKAFNVDVQFKSKMPIQPLNLRVFLCFSNDVSAPVVRCQNHL SVEPLT
gi|25009887|gb|AAN71112.1|RMNKAFNVDVQFKSKMPIQPLNLRVFLCFSNDVSAPVVRCQNHL SVEPLT
                               *****

gi|21355617|ref|NP_651115.1|ANNAKMRESLLRSENPN SVYCGNAQGKGISERFSVVVPLNMSRSVTRSG L
gi|25009887|gb|AAN71112.1|ANNAKMRESLLRSENPN SVYCGNAQGKGISERFSVVVPLNMSRSVTRSG L
                               *****

gi|21355617|ref|NP_651115.1|TRQTLAFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVIHVKICTCPKR
gi|25009887|gb|AAN71112.1|TRQTLAFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVIHVKICTCPKR
                               *****

gi|21355617|ref|NP_651115.1|DRIQDERQLNSKKRKSVP EAAEEDEPSKVRR CIAIKTEDTESNDSRDCDD
gi|25009887|gb|AAN71112.1|DRIQDERQLNSKKRKSVP EAAEEDEPSKVRR CIAIKTEDTESNDSRDCDD
                               *****

gi|21355617|ref|NP_651115.1|SAAEWNVSRTPDGDYRLAITCPNKEWLLQSI EGMIKEAAA EVL RNP NQEN
gi|25009887|gb|AAN71112.1|SAAEWNVSRTPDGDYRLAITCPNKEWLLQSI EGMIKEAAA EVL RNP NQEN
                               *****

gi|21355617|ref|NP_651115.1|LRRHANKLLSLKKRAYELP
gi|25009887|gb|AAN71112.1|LRRHANKLLSLKKRAYELP
                               *****
```

- ☐ Change sequences
- ☐ Align subset of sequences
- ☐ Use Alignment Viewer (new!)
- ☐ Use Tree Viewer (new!)
- ☐ Boxshade ClustalW Alignment (HTML)
- ☐ Boxshade ClustalW Alignment (PostScript)





Nucleotide

Protein

formatting **BLAST**

Translations

Retrieve results for an  
RID

Your request has been successfully submitted and put into the Blast Queue.

Query = gi|31207283|ref|XP\_312608.1| ENSANGP00000014785 [Anopheles gambiae] (338 letters)

Putative conserved domains have been detected, click on the image below for detailed results.



The request ID is 1060208428-027529-6850

**Format!** or **Reset all**

The results are estimated to be ready in 4 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi  in

Number of: Descriptions  Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

Limit results by  or select from:

Expect value range:

EXHIBIT D



## results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

**Ref rence:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1060208428-027529-6850

**Query=** gi|31207283|ref|XP\_312608.1| ENSANGP00000014785  
[Anopheles gambiae]  
(338 letters)

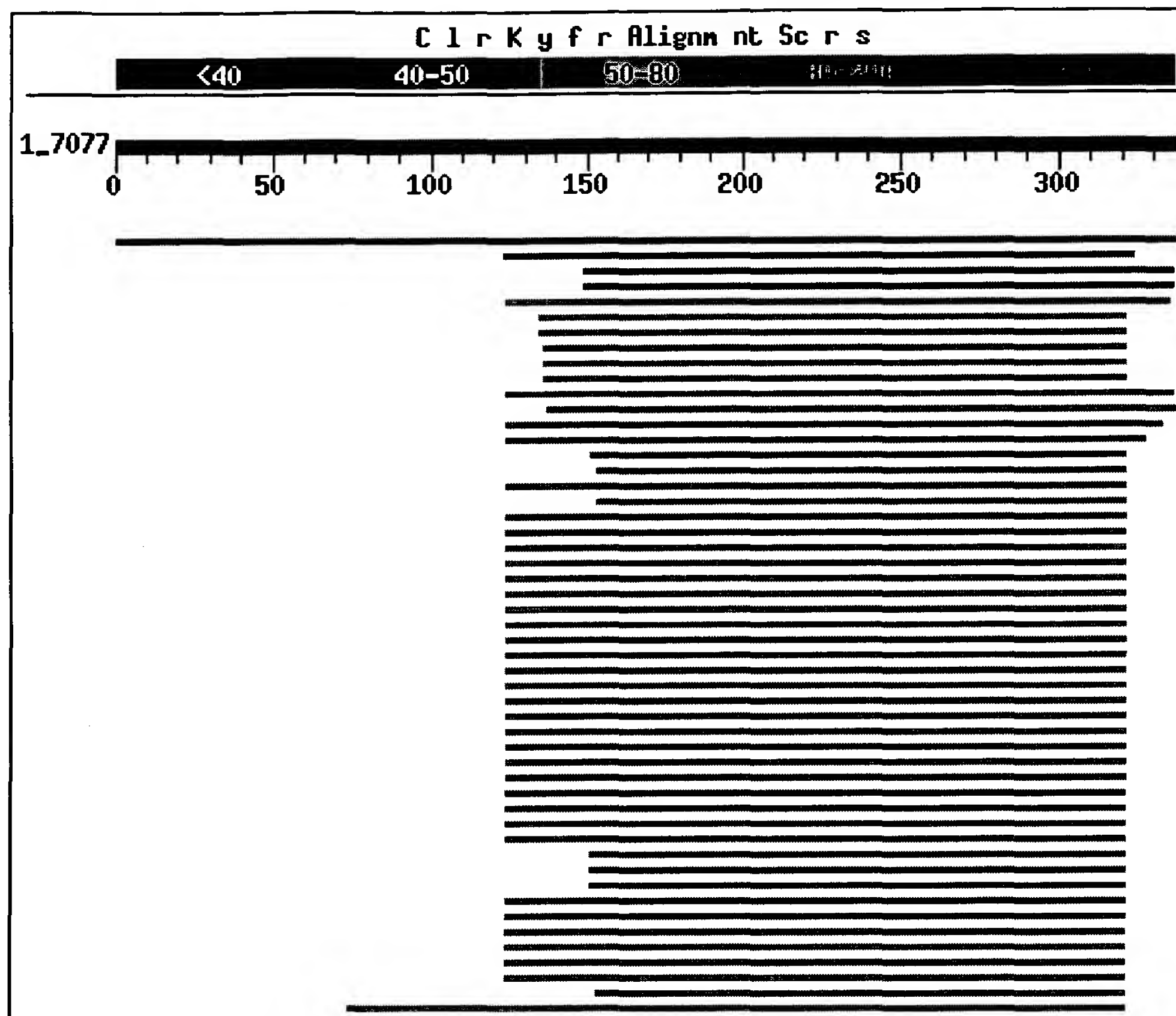
**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,486,004 sequences; 478,769,834 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

### Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



# Related Structures

Sequences producing significant alignments:			Score (bits)	E Value
gi 31207283 ref XP_312608.1	ENSANGP00000014785 [Anopheles ...		692	0.0
gi 31209247 ref XP_313590.1	ENSANGP00000013376 [Anopheles ...		114	2e-24
gi 21355617 ref NP_651115.1	CG10873-PA [Drosophila melanog...		97	3e-19 <b>L</b>
gi 25009887 gb AAN71112.1	AT28346p [Drosophila melanogaster]		97	3e-19
gi 2811079 sp O12946 P53_PLAFE	Cellular tumor antigen p53 (...)		74	5e-12
gi 1244764 gb AAA98564.1	p53 tumor suppressor homolog		73	6e-12
gi 1244762 gb AAA98563.1	p53 tumor suppressor homolog		73	6e-12
gi 19850152 gb AAL99584.1 AF285104_1	p53-like transcription...		69	1e-10
gi 7689271 gb AAF67733.1 AF253323_1	p53 tumor suppressor-li...		69	1e-10
gi 7689273 gb AAF67734.1 AF253324_1	p73-like protein [Mya a...		69	1e-10
gi 10720196 sp Q9W679 P53_TETMU	Cellular tumor antigen p53 ...		67	3e-10
gi 129372 sp P10361 P53_RAT	Cellular tumor antigen p53 (Tum...		67	4e-10 <b>L</b>
gi 18997097 gb AAL83290.1 AF475081_1	P53 [Delphinapterus le...		66	7e-10
gi 1000577 gb AAB42022.1	p53 [Canis familiaris]		66	7e-10
gi 29470179 gb AAO74632.1	p73 [Danio rerio]		66	7e-10
gi 129368 sp P10360 P53_CHICK	Cellular tumor antigen p53 (T...		66	7e-10
gi 15072750 emb CAC48053.1	p63 delta [Homo sapiens]		66	9e-10
gi 10720186 sp Q9TUB2 P53_PIG	Cellular tumor antigen p53 (T...		66	1e-09
gi 7248450 gb AAF43491.1	p51 isoform delNalpha [Homo sapiens]		65	1e-09
gi 13751173 emb CAC37098.1	TA1 KET alpha protein [Rattus n...		65	1e-09 <b>L</b>
gi 13751175 emb CAC37099.1	DN KET alpha protein [Rattus no...		65	1e-09 <b>L</b>

gi 3695094 gb AAC62641.1	TA*p63 alpha [Mus musculus] >gi 3...	65	1e-09	L
gi 9507209 ref NP_062094.1	transformation related protein ...	65	1e-09	L
gi 3510330 dbj BAA32593.1	p51B [Homo sapiens] >gi 7248446 ...	65	1e-09	L
gi 3644040 gb AAC43038.1	CUSP [Homo sapiens] >gi 3695084 g...	65	1e-09	L
gi 31543818 ref NP_003713.3	tumor protein p73-like; tumor ...	65	1e-09	L
gi 13751185 emb CAC37104.1	TA1 KET beta protein [Rattus no...	65	1e-09	L
gi 3695082 gb AAC62635.1	TA p63 alpha [Homo sapiens]	65	1e-09	L
gi 7248451 gb AAF43492.1	p51 isoform delNbeta [Homo sapiens]	65	1e-09	
gi 3970717 emb CAA76562.1	KET protein [Homo sapiens]	65	1e-09	L
gi 6755883 ref NP_035771.1	transformation related protein ...	65	1e-09	L
gi 7248447 gb AAF43488.1	p51 isoform TAp63beta [Homo sapiens]	65	1e-09	
gi 13751187 emb CAC37105.1	DN KET beta protein [Rattus nor...	65	1e-09	L
gi 4996230 dbj BAA78379.1	P53 [Canis familiaris]	65	1e-09	
gi 6093639 sp Q29537 P53_CANFA	Cellular tumor antigen p53 (...)	65	1e-09	
gi 13751183 emb CAC37103.1	TA2 KET beta protein [Rattus no...	65	1e-09	L
gi 12024745 gb AAG45608.1	TA p63 beta [Homo sapiens]	65	1e-09	
gi 3695090 gb AAC62639.1	TA*p63 gamma [Mus musculus] >gi 3...	65	1e-09	L
gi 3695088 gb AAC62638.1	DN p63 beta [Homo sapiens] >gi 12...	65	1e-09	L
gi 13751177 emb CAC37100.1	TA1 KET gamma protein [Rattus n...	65	1e-09	L
gi 3695086 gb AAC62637.1	TA p63 beta [Homo sapiens]	65	1e-09	L
gi 3695092 gb AAC62640.1	TA*p63 beta [Mus musculus] >gi 32...	65	1e-09	L
gi 1463021 gb AAC37335.1	p53 [Canis familiaris]	65	1e-09	
gi 13751181 emb CAC37102.1	DN KET gamma protein [Rattus no...	65	2e-09	L
gi 3695096 gb AAC62642.1	DN p63 gamma [Mus musculus] >gi 3...	65	2e-09	L
gi 3695098 gb AAC62643.1	DN p63 beta [Mus musculus] >gi 32...	65	2e-09	L
gi 13751179 emb CAC37101.1	TA2 KET gamma protein [Rattus n...	65	2e-09	L
gi 12643523 sp Q9XSK8 P73_CERAE	Tumor protein p73 (p53-like...	65	2e-09	
gi 3273745 gb AAC24830.1	p53 homolog [Homo sapiens]	65	2e-09	L
gi 2842672 sp Q64662 P53_SPEBE	Cellular tumor antigen p53 (...)	65	2e-09	
gi 26339452 dbj BAC33397.1	unnamed protein product [Mus mu...	65	2e-09	
gi 3695080 gb AAC62634.1	DN p63 gamma [Homo sapiens] >gi 7...	65	2e-09	L
gi 3510328 dbj BAA32592.1	p51A [Homo sapiens] >gi 3695078 ...	65	2e-09	L
gi 12024746 gb AAG45609.1	TA p63 gamma [Homo sapiens]	65	2e-09	
gi 5353744 gb AAD42225.1	p53 protein [Canis familiaris]	65	2e-09	
gi 7248448 gb AAF43489.1	p51 isoform TAp63delta [Homo sapi...	65	2e-09	
gi 7248452 gb AAF43493.1	p51 isoform delNdelta [Homo sapiens]	65	2e-09	
gi 11342599 emb CAC17147.1	transformation related protein ...	65	2e-09	L
gi 4803651 emb CAA72225.1	P73 splice variant [Cercopithec...	65	2e-09	
gi 23308685 ref NP_689454.1	deltaNp63 isoform alpha 2; tum...	65	2e-09	L
gi 23308709 ref NP_694518.1	deltaNp63 isoform alpha 1; tum...	65	2e-09	L
gi 2833362 sp Q29480 P53_EQUAS	Cellular tumor antigen p53 (...)	64	2e-09	
gi 1938365 gb AAB80959.1	mutant p53 [Rattus norvegicus]	64	3e-09	L
gi 1389675 gb AAB18936.1	tumor-suppressor [Equus caballus]	64	3e-09	
gi 13195250 gb AAK15622.1 AF314148_1	p63 DNA binding protei...	64	3e-09	
gi 19909981 dbj BAB87244.1	deltaN p73 alpha [Homo sapiens]...	64	3e-09	L
gi 20850793 ref XP_131858.1	transformation related protein...	64	3e-09	L
gi 7320915 emb CAB81954.1	P73 delta-N protein [Mus musculus]	64	3e-09	L
gi 12060487 dbj BAB20631.1	DN p63 alpha [Gallus gallus]	64	3e-09	
gi 2370178 emb CAA72221.1	P73 [Homo sapiens]	64	3e-09	L

gi 19909983 dbj BAB87245.1	deltaN p73 beta [Homo sapiens] ...	64	3e-09	L
gi 4885645 ref NP_005418.1	tumor protein p73; p53-related ...	64	3e-09	L
gi 2370177 emb CAA72219.1	P73 [Homo sapiens]	64	3e-09	L
gi 20428532 gb AAK81886.1	DN p73 gamma [Homo sapiens]	64	3e-09	L
gi 10720193 sp Q92143 P53_XIPMA	Cellular tumor antigen p53 ...	64	3e-09	
gi 14719450 pdb 1HU8 A	Chain A, Crystal Structure Of The Mo...	64	4e-09	S
gi 1836145 gb AAB46899.1	sequence-specific transcription f...	64	4e-09	
gi 26348179 dbj BAC37729.1	unnamed protein product [Mus mu...	64	4e-09	L
gi 23308711 ref NP_694519.1	deltaNp63 isoform gamma; tumor...	64	4e-09	L
gi 2829679 sp P79892 P53_HORSE	Cellular tumor antigen p53 (...)	64	5e-09	
gi 10720191 sp O57538 P53_XIPHE	Cellular tumor antigen p53 ...	64	5e-09	
gi 481535 pir S38824	cellular tumor antigen p53, minor spl...	64	5e-09	L
gi 4689086 gb AAD27752.1 AF043641_1	p73 [Barbus barbus]	64	5e-09	
gi 10720192 sp O93379 P53_ICTPU	Cellular tumor antigen p53 ...	64	5e-09	
gi 10720195 sp Q9W678 P53_BARBU	Cellular tumor antigen p53 ...	64	5e-09	
gi 1813455 gb AAB41833.1	p53	64	5e-09	
gi 1813451 gb AAB41831.1	p53	64	5e-09	
gi 28975327 gb AAO60156.1	tumor suppressor p53; p53as [Mus...	63	5e-09	L
gi 13591878 ref NP_112251.1	tumor protein p53; tumor prote...	63	6e-09	L
gi 1813453 gb AAB41832.1	p53	63	6e-09	
gi 53571 emb CAA25323.1	unnamed protein product [Mus muscu...	63	6e-09	L
gi 29468129 gb AAO85406.1 AF365873_1	tumor suppressor p53 [...]	63	6e-09	L
gi 6755881 ref NP_035770.1	transformation related protein ...	63	6e-09	L
gi 129371 sp P02340 P53_MOUSE	Cellular tumor antigen p53 (T...	63	7e-09	L
gi 15375072 gb AAK94783.1	transformation related protein 5...	63	7e-09	L
gi 3445484 dbj BAA32433.1	p73H [Homo sapiens]	63	8e-09	L
gi 1813457 gb AAB41834.1	p53	63	9e-09	
gi 2961247 gb AAC05704.1	tumor suppressor p53 [Mus musculus]	62	1e-08	L
gi 18859503 ref NP_571402.1	tumor protein p53; tumor suppr...	62	1e-08	L
gi 12856636 dbj BAB30732.1	unnamed protein product [Mus mu...	62	1e-08	L

#### Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|31207283|ref|XP\_312608.1| ENSANGP00000014785 [Anopheles gambiae]  
gi|21295812|gb|EAA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PEST]  
Length = 338

Score = 692 bits (1786), Expect = 0.0  
Identities = 338/338 (100%), Positives = 338/338 (100%)

Query: 1 MGEKLATSVIECDLCVPRCESDHVVIKSSFIRSYAMASNMEMLNGEIFGDINTALYQNGE 60  
MGEKLATSVIECDLCVPRCESDHVVIKSSFIRSYAMASNMEMLNGEIFGDINTALYQNGE  
Sbjct: 1 MGEKLATSVIECDLCVPRCESDHVVIKSSFIRSYAMASNMEMLNGEIFGDINTALYQNGE 60

Query: 61 DCQSLFRMNTNDLLPQQGSDLSELMLNDFHNGVAEMQCVKYETDAKLLTMLDGREEPT 120  
DCQSLFRMNTNDLLPQQGSDLSELMLNDFHNGVAEMQCVKYETDAKLLTMLDGREEPT  
Sbjct: 61 DCQSLFRMNTNDLLPQQGSDLSELMLNDFHNGVAEMQCVKYETDAKLLTMLDGREEPT 120



Query: 121 HYKKIPVLDDFTHPLLQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDVTYMQPSD 180  
 HYKKIPVLDDFTHPLLQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDVTYMQPSD  
 Sbjct: 121 HYKKIPVLDDFTHPLLQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDVTYMQPSD 180

Query: 181 YSRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCCLNPASFTGREKGV 240  
 YSRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCCLNPASFTGREKGV  
 Sbjct: 181 YSRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCCLNPASFTGREKGV 240

Query: 241 NFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSCPTMERRATTLVFTVENEHGT 300  
 NFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSCPTMERRATTLVFTVENEHGT  
 Sbjct: 241 NFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSCPTMERRATTLVFTVENEHGT 300

Query: 301 LGRKSISVKICSCPGRDMEKDDSKATGGRENNKNKRKH 338  
 LGRKSISVKICSCPGRDMEKDDSKATGGRENNKNKRKH  
 Sbjct: 301 LGRKSISVKICSCPGRDMEKDDSKATGGRENNKNKRKH 338

☐ >gi|31209247|ref|XP\_313590.1| ENSANGP00000013376 [Anopheles gambiae]  
 gi|21296914|gb|EAA09059.1| ENSANGP00000013376 [Anopheles gambiae str. PEST]  
 Length = 332

Score = 114 bits (286), Expect = 2e-24  
 Identities = 69/207 (33%), Positives = 112/207 (54%), Gaps = 19/207 (9%)

Query: 124 KIPVLDDFTHPLLQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDV-----TYMQP 178  
 K P +D+ + F V S S + +S L+KLF+K + +FD+ T++ P  
 Sbjct: 105 KYPSVDELCPADIHFTVIPSS--QGS GFIFSEQLQKLFLKTDSICSFDIACQLPTFLPP 162

Query: 179 SDYSRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCCLNPASFTGREK 238  
 + + +R+MLV + +++I+RC IA D + K HVVRC N + G +  
 Sbjct: 163 TGWY---VRVMLVSLAPESQHESITRCHKHIAHDTGPEEIRK-HVVRCCKNEQHEYVGADN 218

Query: 239 GVNFEEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSCPTMERRATTLVFTVENEHG 298  
 G FEDR AV V L+ ++ V + L+F+CQN+C +++R T LVFT+EN+ G  
 Sbjct: 219 GPFFEDRYAVRVPLD-----DEVLCVKIMLQFVCQNTCFRLDQRRGTGLVFTLENDQG 270

Query: 299 TLLGRKSISVKICSCPGRDMEKDDSKA 325  
 + R+ + VKIC +RDM+ + + A  
 Sbjct: 271 NIWARRVVPVKICINYRRDMQNEQNSA 297

☐ >gi|21355617|ref|NP\_651115.1| ☒ CG10873-PA [Drosophila melanogaster]  
 gi|7211767|gb|AAF40427.1|AF224713\_1 ☒ transcription factor p53 [Drosophila melano  
 gi|7211769|gb|AAF40428.1|AF224714\_1 ☒ transcription factor p53 [Drosophila melano  
 gi|7381624|gb|AAF61572.1|AF244918\_1 ☒ p53 tumor suppressor-like protein [Drosophi  
 gi|8272608|gb|AAF74277.1|AF250918\_1 ☒ transcription factor [Drosophila melanogast  
 gi|8453176|gb|AAF75270.1|AF263722\_1 ☒ transcription factor p53 [Drosophila melano  
 gi|10726710|gb|AAF56087.2| ☒ CG10873-PA [Drosophila melanogaster]  
 gi|17861528|gb|AAL39241.1| ☒ GH11591p [Drosophila melanogaster]  
 gi|18032162|gb|AAL56639.1|AF192555\_1 p53-like regulator of apoptosis and cell cyc  
 melanogaster]  
 Length = 385

Score = 97.4 bits (241), Expect = 3e-19  
 Identities = 64/192 (33%), Positives = 102/192 (53%), Gaps = 17/192 (8%)

Query: 150 SAWCYSNALEKLFVKKKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRCQDDI 209  
 S W YS L KL+++ DV + L LR+ L +SN A + RCQ+ +  
 Sbjct: 103 SLWMYSIPLNKLYIRMNKA FNVDVQFKSKMPIQPLNLRVFLCFSNDVSA--PVVRCQNHL 160

Query: 210 AKD--GAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLN--NGGTPQHLEKQQ 265  
 + + A + +E ++R NP++ + G +G +R +V+V LN T L +Q  
 Sbjct: 161 SVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQT 220

Query: 266 TVPVSLEFLCQNSCPTMERRATTLVFTVENEHGTLGRKSISVKICSCPKRDMEKDDSKA 325  
 ++ +F+CQNSC + R+ T+LVF +E G ++G+ I VKIC+CPKRD +D+  
 Sbjct: 221 ---LAFKFVCQNSC--IGRKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIQDE--- 272

Query: 326 TGGRENNKNKRK 337  
 R+ N KRK  
 Sbjct: 273 ---RQLNSKKRK 281

☐ >gi|25009887|gb|AAN71112.1| AT28346p [Drosophila melanogaster]  
 Length = 519

Score = 97.4 bits (241), Expect = 3e-19  
 Identities = 64/192 (33%), Positives = 102/192 (53%), Gaps = 17/192 (8%)

Query: 150 SAWCYSNALEKLFVKKKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRCQDDI 209  
 S W YS L KL+++ DV + L LR+ L +SN A + RCQ+ +  
 Sbjct: 237 SLWMYSIPLNKLYIRMNKA FNVDVQFKSKMPIQPLNLRVFLCFSNDVSA--PVVRCQNHL 294

Query: 210 AKD--GAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLN--NGGTPQHLEKQQ 265  
 + + A + +E ++R NP++ + G +G +R +V+V LN T L +Q  
 Sbjct: 295 SVEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQT 354

Query: 266 TVPVSLEFLCQNSCPTMERRATTLVFTVENEHGTLGRKSISVKICSCPKRDMEKDDSKA 325  
 ++ +F+CQNSC + R+ T+LVF +E G ++G+ I VKIC+CPKRD +D+  
 Sbjct: 355 ---LAFKFVCQNSC--IGRKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIQDE--- 406

Query: 326 TGGRENNKNKRK 337  
 R+ N KRK  
 Sbjct: 407 ---RQLNSKKRK 415

☐ >gi|2811079|sp|O12946|P53\_PLAFE Cellular tumor antigen p53 (Tumor suppressor p53)  
 gi|1922902|emb|CAA70123.1| p53 [Platichthys flesus]  
 Length = 366

Score = 73.6 bits (179), Expect = 5e-12  
 Identities = 58/220 (26%), Positives = 100/220 (45%), Gaps = 23/220 (10%)

Query: 125 IPVLDDEFTHPL-LQFNVAISGKPCSASAWCYSNALEKLFV--KKTPVTFDVTYMQPSDY 181  
 +PV+ D+ Q SG S ++ +S L+KL+ + K +PV ++ P  
 Sbjct: 75 VPVVTDYPGGEYGFQLRQKSGTAKSVTS-TFSELLKKLYCQLAKTSPVEVLLSKEPPQGA 133

Query: 182 SRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAHKEHVVRCLNPDASFTGREKGVN 241  
 LR VY +++ + RC +D A+ H+ H++R G ++ +  
 Sbjct: 134 V---LRATAVYKKTEHVADVVRRCPPHHQTEDTAE---HRSHLIR-----LEGSQRALY 180

Query: 242 FEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTL 300

FED + P L +T + L F+C +SC M RR + T+E G +  
 Sbjct: 181 FEDPHTKRQSVTVPYEPPQL-GSETTAILLSFMCNSSCMGGMNRRQILTILLETDPGLV 239

Query: 301 LGRKSISVKICSCPGRDMEKDDSKAT----GGRENNKNKR 336  
 LGR+ V++C+CP RD + D+ +T G ++ K K+

Sbjct: 240 LGRRCFEVRVCACPRDRKTDEESSTKTPNGPKQTKKRKQ 279

☐ >gi|1244764|gb|AAA98564.1| p53 tumor suppressor homolog  
 Length = 391

Score = 73.2 bits (178), Expect = 6e-12  
 Identities = 54/194 (27%), Positives = 95/194 (48%), Gaps = 21/194 (10%)

Query: 135 LLQFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVY 192  
 + + + A K ++ W YS L+KL+V+ T PV F PS ++R M +Y

Sbjct: 133 VFEMSFAQPSKETKSTTWTYSEKLDKLYVRMATTCPVRFKTARPPPSG---CQIRAMPIY 189

Query: 193 SNSQYAYQTISRCQDD-IAKDGAKEHVRCLNPDASFTGREKGVNFEDRLAVLVD 251  
 ++ + + RC + AK+ + H+VRC + A + + + R +VL+

Sbjct: 190 MKPEHVQEVVKRCPNHATAKEHNEKHPAPLHIVRCEHKLAKYHEDK----YSGRQSVLI- 244

Query: 252 LNNGGTPQHLEK--QQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISV 308  
 P + + + V +F+C SC RR LVFT+E ++ +LGR+++ V

Sbjct: 245 -----PHEMPQAGSEWVNLYQFMCLGSCVGGPNRRPIQLVFTLEKDN-QVLGRRAVEV 297

Query: 309 KICSCPGRDMEKDD 322  
 +IC+CP RD + D+

Sbjct: 298 RICACPRDRKADE 311

☐ >gi|1244762|gb|AAA98563.1| p53 tumor suppressor homolog  
 Length = 564

Score = 73.2 bits (178), Expect = 6e-12  
 Identities = 54/194 (27%), Positives = 95/194 (48%), Gaps = 21/194 (10%)

Query: 135 LLQFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVY 192  
 + + + A K ++ W YS L+KL+V+ T PV F PS ++R M +Y

Sbjct: 133 VFEMSFAQPSKETKSTTWTYSEKLDKLYVRMATTCPVRFKTARPPPSG---CQIRAMPIY 189

Query: 193 SNSQYAYQTISRCQDD-IAKDGAKEHVRCLNPDASFTGREKGVNFEDRLAVLVD 251  
 ++ + + RC + AK+ + H+VRC + A + + + R +VL+

Sbjct: 190 MKPEHVQEVVKRCPNHATAKEHNEKHPAPLHIVRCEHKLAKYHEDK----YSGRQSVLI- 244

Query: 252 LNNGGTPQHLEK--QQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISV 308  
 P + + + V +F+C SC RR LVFT+E ++ +LGR+++ V

Sbjct: 245 -----PHEMPQAGSEWVNLYQFMCLGSCVGGPNRRPIQLVFTLEKDN-QVLGRRAVEV 297

Query: 309 KICSCPGRDMEKDD 322  
 +IC+CP RD + D+

Sbjct: 298 RICACPRDRKADE 311

☐ >gi|19850152|gb|AAL99584.1|AF285104\_1 p53-like transcription factor p120 [Spisu]  
 Length = 591

Score = 68.9 bits (167), Expect = 1e-10

Identities = 51/190 (26%), Positives = 93/190 (48%), Gaps = 17/190 (8%)

Query: 137 QFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVYSN 194  
 + + A K ++ W YS+ L+KL+V+ T PV F P+ +R M ++

Sbjct: 143 EISFATPSKETKSTTWTYSDDLKLYVRMATTCPVRFKTNRQPPAG---CIIRSMPIFMK 199

Query: 195 SQYAYQTISRCQDD-IAKDGAKEFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVLDN 253  
 ++ + + RC + +K+ ++ H+VRC + A + + R +V++

Sbjct: 200 PEHVQEAVKRCPNHATSKEFNENHPAPNHLVRCEHKLAKYVEDP----YTSRQSVVIPQE 255

Query: 254 NGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICS 312  
 TPQ + V +F+C SC RR +VFT+E ++ +LGR+ + V+IC+

Sbjct: 256 ---TPQ--AGSEWVTNLFQFMCLGSCVGGPNRRPLQIVFTLEKDN-QVLGRRRCVEVRICA 309

Query: 313 CPKRDMEKDD 322

CP RD + D+

Sbjct: 310 CPGDRDRKGDE 319

☐ >gi|7689271|gb|AAF67733.1|AF253323\_1 p53 tumor suppressor-like protein [Mya areer  
 Length = 443

Score = 68.9 bits (167), Expect = 1e-10

Identities = 51/190 (26%), Positives = 93/190 (48%), Gaps = 17/190 (8%)

Query: 137 QFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVYSN 194  
 + + A K ++ W YS+ L+KL+V+ T PV F P +R M ++

Sbjct: 149 EISFATPSKETKSTTWTYSDDLKLYVRMATTCPVRFKTLRQPPPG---CVIRSMPIFMK 205

Query: 195 SQYAYQTISRCQDD-IAKDGAKEFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVLDN 253  
 ++ + + RC + +K+ ++ H+VRC + + + + +R +VL+

Sbjct: 206 PEHVQEAVKRCPNHATSKEFNENHPAPNHLVRCEHKVSKYVEDP----YTNRQSVLIPQE 261

Query: 254 NGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICS 312  
 TPQ + V +F+C SC RR +VFT+E ++ +LGR+ + V+IC+

Sbjct: 262 ---TPQ--AGSEWVTNLFQFMCLGSCVGGPNRRPLQIVFTLEKDN-QVLGRRRCVEVRICA 315

Query: 313 CPKRDMEKDD 322

CP RD + D+

Sbjct: 316 CPGDRDKADE 325

☐ >gi|7689273|gb|AAF67734.1|AF253324\_1 p73-like protein [Mya arenaria]  
 Length = 621

Score = 68.6 bits (166), Expect = 1e-10

Identities = 51/190 (26%), Positives = 93/190 (48%), Gaps = 17/190 (8%)

Query: 137 QFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVYSN 194  
 + + A K ++ W YS+ L+KL+V+ T PV F P +R M ++

Sbjct: 149 EISFATPSKETKSTTWTYSDDLKLYVRMATTCPVRFKTLRQPPPG---CVIRSMPIFMK 205

Query: 195 SQYAYQTISRCQDD-IAKDGAKEFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVLDN 253  
 ++ + + RC + +K+ ++ H+VRC + + + + +R +VL+

Sbjct: 206 PEHVQEAVKRCPNHATSKEFNENHPAPNHLVRCEHKVSKYVEDP----YTNRQSVLIPQE 261

Query: 254 NGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLGRKSISVKICS 312  
 TPQ + V +F+C SC RR +VFT+E ++ +LGR+ + V+IC+  
 Sbjct: 262 ---TPQ--AGSEWVTNLFQFMCLGSCVGGPNRRPLQIVFTLEKDN-QVLGRRCVEVRICA 315

Query: 313 CPKRDMEKDD 322  
 CP RD + D+  
 Sbjct: 316 CPGDRKKADE 325

☐ >gi|10720196|sp|Q9W679|P53\_TETMU Cellular tumor antigen p53 (Tumor suppressor p53)  
 gi|4959052|gb|AAD34213.1|AF071571\_1 tumor suppressor protein p53 [Tetraodon miuru]  
 Length = 367

Score = 67.4 bits (163), Expect = 3e-10  
 Identities = 52/217 (23%), Positives = 99/217 (45%), Gaps = 19/217 (8%)

Query: 125 IPVLDLDFTHPL---LQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDVTYMQPSDY 181  
 +PV D+ L+F + + K +++ YS L KL+ + +V +  
 Sbjct: 81 VPVTTDYPGEYGFKLRFQKSGTAKSVTST---YSEILNKLYCQLAKTSLVEVLLGKDPPM 137

Query: 182 SRLKLRLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCLNPDASFTGREKGVN 241  
 + LR +Y +++ + + RC +D A+ H+ H++R G E+  
 Sbjct: 138 GAV-LRATAIYKKTEHVAEVRRCPHHQNEDSAE---HRSHLIR-----MEGSERAQY 186

Query: 242 FEDRLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTL 300  
 FE + P L + T + L F+C +SC M RR + T+E + G +  
 Sbjct: 187 FEHPHTKRQSVTPYEPPLGSEFTT-ILLSFMCNSSCMGGMNRRPILTILTLETQEGIV 245

Query: 301 LGRKSISVKICSCP KRDMEKDDSKATGGRENNKNKRK 337  
 LGR+ V++C+CP RD + +++ +T + + K+ +K  
 Sbjct: 246 LGRRCFEVRVCACPGDRKTEETNSTKMQNDADAKK 282

☐ >gi|129372|sp|P10361|P53\_RAT Cellular tumor antigen p53 (Tumor suppressor p53)  
 gi|92070|pir|S02192 cellular tumor antigen p53 - rat  
 gi|56829|emb|CAA31457.1| **L** unnamed protein product [Rattus norvegicus]  
 Length = 391

Score = 67.0 bits (162), Expect = 4e-10  
 Identities = 56/206 (27%), Positives = 89/206 (43%), Gaps = 24/206 (11%)

Query: 138 FNVAISGKPCSASAWC-YNALEKLFVK--KKTPTVTFDVTYMQPSDYSRLKLRLVYSN 194  
 F++ + S C YS +L KLF + K PV VT P ++R M +Y  
 Sbjct: 107 FHLGFLQSGTAKSVMCTYSISLNKLFQQLAKTQCPVQLWVTSTPPPG---TRVRAMAIYKK 163

Query: 195 SQYAYQTISRCQDDIAKDGAKEHVVRCL-NPDASFTGREKGVNFEDRLAVLVLDL 253  
 SQ+ + + RC A +H++R NP A + +DR +  
 Sbjct: 164 SQHMTEVVRRCPHHERCSDGDGLAPPQHILIRVEGNPYAEY-----LDDRQTFRHSVV 215

Query: 254 NGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLGRKSISVKICS 312  
 P + T + +++C +SC M RR + T+E+ G LLGR S V++C+  
 Sbjct: 216 VPYEPPEVGSDYTT-IHYKYMNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCA 274

Query: 313 CPKRDMEKDDSKATGGRENNKNKRKH 338  
 CP RD ++ EN + K +H  
 Sbjct: 275 CPGDRRTEE-----ENFRKKEEH 293

☐ >gi|18997097|gb|AAL83290.1|AF475081\_1 P53 [Delphinapterus leucas]  
Length = 387

Score = 66.2 bits (160), Expect = 7e-10  
Identities = 49/173 (28%), Positives = 78/173 (45%), Gaps = 15/173 (8%)

Query: 154 YSNALEKLFVK--KKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDDIA 210  
YS AL KLF + K PV V+ P ++R M +Y S+Y + + RC +  
Sbjct: 119 YSPALNKLFCQLAKTCPVQLWVSSPPPPG---TRVRAMAIYKKSEYMTEVVRRCPHHERC 175

Query: 211 KDGAKEFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVPVS 270  
D + A +H++R G + +DR + P + T +  
Sbjct: 176 SDYSDGLAPPQHLIRV-----EGNLRAEYLDDRNTFRHSVVPYEPPEVGSDCTT-IH 227

Query: 271 LEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPGRDMEKDD 322  
F+C +SC M RR + T+E+ +G LLGR S V++C+CP RD ++  
Sbjct: 228 YNFMCNSSCMGGMNRRPILTIITLEDSSGNLGRNSFEVRVCACPGRDRRTEE 280

☐ >gi|1000577|gb|AAB42022.1| p53 [Canis familiaris]  
Length = 276

Score = 66.2 bits (160), Expect = 7e-10  
Identities = 46/175 (26%), Positives = 77/175 (44%), Gaps = 15/175 (8%)

Query: 152 WCYSNALEKLFVK--KKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDD 208  
W YS L KLF + K PV V+ P + +R M +Y S++ + + RC +  
Sbjct: 87 WTYSPLLNLKFCQLAKTCPVQLWVSSPPPPNTC---VRAMAIYKKSEFVTEVVRRCPHHE 143

Query: 209 IAKDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVP 268  
D + A +H++R G + +DR + P + T  
Sbjct: 144 RCSDSSDGLAPPQHLIRV-----EGNLRAKYLLDDRNTFRHSVVPYEPPEVGSDYTT- 195

Query: 269 VSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPGRDMEKDD 322  
+ ++C +SC M RR + T+E+ G +LGR S V++C+CP RD ++  
Sbjct: 196 IHYNYMCNSSCMGGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPGRDRRTEE 250

☐ >gi|29470179|gb|AA074632.1| p73 [Danio rerio]  
Length = 640

Score = 66.2 bits (160), Expect = 7e-10  
Identities = 63/233 (27%), Positives = 101/233 (43%), Gaps = 41/233 (17%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLF--VKKKTPVTFDVTYMQPSDY 181  
IP D+ P F V + SA W YS L+KL+ + K P+ + P+  
Sbjct: 122 IPSNTDYPGP-HNFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKLASSPPNGS 180

Query: 182 SRLKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVR-----CLNPDASF 233  
+R M +Y +++ + + RC + + +D A H++R C D  
Sbjct: 181 V---IRAMPIYKKAHEVTEVVKRCPNHKLGRDFNESQTAPASHLIRVEGNNLCQYVDDPV 237

Query: 234 TGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFT 292  
TGR+ +VLV +PQ + T+ + F+C +SC M RR ++ T



Sbjct: 238 TGRQ-----SVLVPYE---SPQVGTEFTTILYN--FMCNSSCVGGMNRRPILIIIT 283

Query: 293 VENEHGTLLGRKSISVKICSCPGRDMEKD-----DSKATGGRENNKN 334

+E G +LGR+S +IC+CP RD + D +S A G N +N

Sbjct: 284 LETRDGQVLGRRSFEGRICACPGDRKADHDHFREQQALNESVAKNGNANKRN 336

☐ >gi|129368|sp|P10360|P53\_CHICK Cellular tumor antigen p53 (Tumor suppressor p53)  
 gi|86220|pir|S02193 cellular tumor antigen p53 - chicken  
 gi|63741|emb|CAA31456.1| nuclear protein p53 (AA 1 - 367) [Gallus gallus]  
 Length = 367

Score = 66.2 bits (160), Expect = 7e-10

Identities = 61/212 (28%), Positives = 93/212 (43%), Gaps = 21/212 (9%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASAWC-YSNALEKLFVK--KKTPTVTFDVTYMQPSDY 181

+P +D+ F V + S C YS L K++ + K PV V P

Sbjct: 82 VPSTEDYGGD-FDFRVGFVEAGTAKSVTCTYSPVLNKVYCRLAKPCPVQVRVGVAPPPGS 140

Query: 182 SRLKLRLIMLVYSNSQYAYQTISRCQDDIAKDGAKE-FAHKEHVVRCL-NPDASFTGREKG 239

S LR + VY S++ + + RC G D A +H++R NP A + E

Sbjct: 141 S---LRAVAVYKKSEHVAEVVRRCPHHERCGGGTDGLAPAQHLIRVEGNPQARYHDDDET- 196

Query: 240 VNFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHG 298

R +V+V P + T V F+C +SC M RR + T+E G

Sbjct: 197 ---TKRHSVVVPYE----PPEVGSDDCTT-VLYNFMCNSSCMGGMNRRPILTILTLEGP GG 248

Query: 299 TLLGRKSISVKICSCPGRD--MEKDDSKATGG 328

LLGR+ V++C+CP RD +E+++ + GG

Sbjct: 249 QLLGRRCFEVRVCACPGDRKIEEENFRKRGG 280

☐ >gi|15072750|emb|CAC48053.1| p63 delta [Homo sapiens]  
 Length = 232

Score = 65.9 bits (159), Expect = 9e-10

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183

IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 13 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 71

Query: 184 LKLRLIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241

+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 72 V-IRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 123

Query: 242 FED---RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296

ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 124 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 178

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 179 DGQVLGRRCFEARICACPGDRKAD 204

☐ >gi|10720186|sp|Q9TUB2|P53\_PIG Cellular tumor antigen p53 (Tumor suppressor p53)

gi|6165623|gb|AAF04620.1|AF098067\_1 tumor suppressor p53 [Sus scrofa]  
Length = 386

Score = 65.9 bits (159), Expect = 1e-09  
Identities = 49/173 (28%), Positives = 78/173 (45%), Gaps = 15/173 (8%)

Query: 154 YSNALEKLFVK--KKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDDIA 210  
YS AL KLF + K PV V+ P ++R M +Y S+Y + + RC + +

Sbjct: 118 YSPALNKLFCQLAKTQPVQLWVSSPPPPG---TRVRAMAIYKKSEYMTEVVRRCPPHERS 174

Query: 211 KDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVPVS 270  
D + A +H++R G + +DR + P + T +

Sbjct: 175 SDYSDGLAPPQHLIRV-----EGNLRAEYLDDRNTFRHSVVVPYEPPEVGSDCTT-IH 226

Query: 271 LEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPGRDMEKDD 322  
F+C +SC M RR + T+E+ G LLGR S V++C+CP RD ++

Sbjct: 227 YNFMCNSSCMGGMNRRPILTIITLEDASGNLLGRNSFEVRVCACPGRRDRTEE 279

☐ >gi|7248450|gb|AAF43491.1| p51 isoform delNalpha [Homo sapiens]  
Length = 586

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDEFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 182 VEDPITGRQSVLPYE---PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLGRKSISVKICSCPGRDMEKDD 322  
G +LGR+ +IC+CP RD + D+

Sbjct: 237 DGQVLGRRCFEARICACPGRRDRKADE 262

☐ >gi|13751173|emb|CAC37098.1| ☒ TA1 KET alpha protein [Rattus norvegicus]  
Length = 663

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDEFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 148 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 206

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 207 V-IRAMPVYKKAHEVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 258

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296



ED R +VLV P + + T V F+C +SC M RR ++ T+E  
Sbjct: 259 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 313

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322  
G +LGR+ +IC+CP RD + D+

Sbjct: 314 DGQVLGRRCFEARICACPGRDRKADE 339

☐ >gi|13751175|emb|CAC37099.1| ☒ DN KET alpha protein [Rattus norvegicus]  
Length = 586

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322  
G +LGR+ +IC+CP RD + D+

Sbjct: 237 DGQVLGRRCFEARICACPGRDRKADE 262

☐ >gi|3695094|gb|AAC62641.1| ☒ TA\*p63 alpha [Mus musculus]  
gi|32812141|gb|AAP87982.1| p63 TA alpha [Mus musculus]  
Length = 680

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 224 V-IRAMPVYKKAHEVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 276 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322  
G +LGR+ +IC+CP RD + D+

Sbjct: 331 DGQVLGRRCFEARICACPGRDRKADE 356

☐ >gi|9507209|ref|NP\_062094.1| ☒ transformation related protein 63; tumor protein

norvegicus]

gi|7630117|emb|CAB88216.1| **L** TA2 KET alpha [Rattus norvegicus]  
Length = 680

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 224 V-IRAMPVYKKAHEVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 276 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 331 DGQVLGRRCFEARICACPGDRKKADE 356

**L** >gi|3510330|dbj|BAA32593.1| **L** p51B [Homo sapiens]

gi|7248446|gb|AAF43487.1| p51 isoform TAp63alpha [Homo sapiens]  
Length = 641

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 126 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 184

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 185 V-IRAMPVYKKAHEVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 236

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 237 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 291

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 292 DGQVLGRRCFEARICACPGDRKKADE 317

**L** >gi|3644040|gb|AAC43038.1| **L** CUSP [Homo sapiens]

gi|3695084|gb|AAC62636.1| **L** DN p63 alpha [Homo sapiens]  
gi|12024747|gb|AAG45610.1| DN p63 alpha [Homo sapiens]  
Length = 586

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183

IP D+ P F+V+ + SA W YS L+KL+ + + M P  
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRI MLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 130 V-IRAMPVYKKA EHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFM CNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTL LGRKSISVKICSCP KRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 237 DGQVLGRRCFEARICACPG RDRKADE 262

☐ >gi|31543818|ref|NP\_003713.3| ☒ tumor protein p73-like; tumor protein 63 kDa wit  
 to p53; tumor protein p63 [Homo sapiens]  
 gi|12024744|gb|AAG45607.1| TA p63 alpha [Homo sapiens]  
 gi|24980977|gb|AAH39815.1| ☒ tumor protein p63 [Homo sapiens]  
 Length = 680

Score = 65.5 bits (158), Expect = 1e-09  
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLD DDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
 IP D+ P F+V+ + SA W YS L+KL+ + + M P  
 Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRI MLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 224 V-IRAMPVYKKA EHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 276 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFM CNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTL LGRKSISVKICSCP KRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 331 DGQVLGRRCFEARICACPG RDRKADE 356

☐ >gi|13751185|emb|CAC37104.1| ☒ TA1 KET beta protein [Rattus norvegicus]  
 Length = 538

Score = 65.5 bits (158), Expect = 1e-09  
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLD DDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
 IP D+ P F+V+ + SA W YS L+KL+ + + M P  
 Sbjct: 148 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 206

Query: 184 LKLRI MLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 207 V-IRAMPVYKKA EHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 258

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296

ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 259 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 313

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 314 DGQVLGRRCFEARICACPGRDRKADE 339

☐ >gi|3695082|gb|AAC62635.1| **L** TA p63 alpha [Homo sapiens]  
 Length = 641

Score = 65.5 bits (158), Expect = 1e-09  
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
 IP D+ P F+V+ + SA W YS L+KL+ + + M P  
 Sbjct: 126 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 184

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 185 V-IRAMPVYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRV-----EGNSHAQY 236

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 237 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 291

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 292 DGQVLGRRCFEARICACPGRDRKADE 317

☐ >gi|7248451|gb|AAF43492.1| p51 isoform delNbeta [Homo sapiens]  
 Length = 461

Score = 65.5 bits (158), Expect = 1e-09  
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
 IP D+ P F+V+ + SA W YS L+KL+ + + M P  
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 237 DGQVLGRRCFEARICACPGRDRKADE 262

☐ >gi|3970717|emb|CAA76562.1| **L** KET protein [Homo sapiens]  
 Length = 680

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 224 V-IRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 276 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 331 DGQVLGRRCFEARICACPGDRKRADE 356

☐ >gi|6755883|ref|NP\_035771.1| **L** transformation related protein 63; KET protein; t  
[Mus musculus]

gi|3445482|dbj|BAA32432.1| **L** p73H [Mus musculus]

gi|3695100|gb|AAC62644.1| **L** DN p63 alpha [Mus musculus]

gi|32812144|gb|AAP87985.1| p63 DN alpha [Mus musculus]

Length = 586

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 237 DGQVLGRRCFEARICACPGDRKRADE 262

☐ >gi|7248447|gb|AAF43488.1| p51 isoform TAp63beta [Homo sapiens]  
Length = 516

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 126 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 184

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G  
Sbjct: 185 V-IRAMPVYKKAHEVTEVVKRCPNHEL SREFNEGQIAPPSHLIRV-----EGNSHAQY 236

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E  
Sbjct: 237 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFM CNSSCVGGMNRRPILIIIVTLETR 291

Query: 297 HGTL LGRKSISVKICSCP KRDMEKDD 322  
G +LGR+ +IC+CP RD + D+  
Sbjct: 292 DGQVLGRRCFEARICACPG RDRKADE 317

☐ >gi|13751187|emb|CAC37105.1| ☒ DN KET beta protein [Rattus norvegicus]  
Length = 461

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLD DFT HPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P  
Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G  
Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHEL SREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E  
Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFM CNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTL LGRKSISVKICSCP KRDMEKDD 322  
G +LGR+ +IC+CP RD + D+  
Sbjct: 237 DGQVLGRRCFEARICACPG RDRKADE 262

☐ >gi|4996230|dbj|BAA78379.1| ☐ P53 [Canis familiaris]  
Length = 381

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 46/175 (26%), Positives = 77/175 (44%), Gaps = 15/175 (8%)

Query: 152 WCYSNALEKLFVK--K KTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDD 208  
W YS L KLF + K PV V+ P + +R M +Y S++ + + RC +  
Sbjct: 111 WTYSPLL NKLFCQLAKTCPVQLWVSSPPPPNTC---VRAMAIYKKSEFVTEVVRRC PHHE 167

Query: 209 IAKDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVP 268  
D + A +H++R G + +DR + P + T  
Sbjct: 168 RCSDSSDGLAPPQHLIRV-----EGNLR AKYLDDRNTFRHSVVVPYEPPEVGSDYTT- 219

Query: 269 VSLEFLCQNSC-PTMERRATTLVFTVENEHGTL LGRKSISVKICSCP KRDMEKDD 322  
+ ++C +SC M RR + T+E+ G +LGR S V++C+CP RD ++  
Sbjct: 220 IHYNYMCNSSCMGGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPG RDRRTEE 274



☐ >gi|6093639|sp|Q29537|P53\_CANFA Cellular tumor antigen p53 (Tumor suppressor p53 protein) [Canis familiaris]  
gi|3150077|gb|AAC16909.1| p53 protein [Canis familiaris]  
Length = 381

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 46/175 (26%), Positives = 77/175 (44%), Gaps = 15/175 (8%)

Query: 152 WCYSNALEKLFVK--KKTPTFTDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDD 208  
W YS L KLF + K PV V+ P + +R M +Y S++ + + RC +  
Sbjct: 111 WTYSPLLNKLFQCLAKTCPVQLWVSSPPPPNTC---VRAMAIYKKSEFVTEVVRRCPHHE 167

Query: 209 IAKDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVP 268  
D + A +H++R G + +DR + P + T  
Sbjct: 168 RCSDSSDGLAPPQHLIRV-----EGNLRKYLDDRNTRHSHVVPYEPPEVGSDYTT- 219

Query: 269 VSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPGRDMEKDD 322  
+ ++C +SC M RR + T+E+ G +LGR S V++C+CP RD ++  
Sbjct: 220 IHNYMCNSSCMGGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPGRRDRTEE 274

☐ >gi|13751183|emb|CAC37103.1| ☒ TA2 KET beta protein [Rattus norvegicus]  
Length = 555

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P  
Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G  
Sbjct: 224 V-IRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED---RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E  
Sbjct: 276 VEDPITGRQSVLPYE---PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLGRKSISVKICSCPGRDMEKDD 322  
G +LGR+ +IC+CP RD + D+  
Sbjct: 331 DGQVLGRRCFEARICACPGRRDRKADE 356

☐ >gi|12024745|gb|AAG45608.1| TA p63 beta [Homo sapiens]  
Length = 555

Score = 65.5 bits (158), Expect = 1e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P  
Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G  
Sbjct: 224 V-IRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIVTLETR 330

Query: 297 HGTLGRKSI SVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 331 DGQVLGRRCFEARICACPRDRKADE 356

☐ >gi|3695090|gb|AAC62639.1| ☒ TA\*p63 gamma [Mus musculus]  
 gi|32812143|gb|AAP87984.1| p63 TA gamma [Mus musculus]  
 Length = 483

Score = 65.5 bits (158), Expect = 1e-09  
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
 IP D+ P F+V+ + SA W YS L+KL+ + + M P  
 Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRI MLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 224 V-IRAMPVYKKA EHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIVTLETR 330

Query: 297 HGTLGRKSI SVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 331 DGQVLGRRCFEARICACPRDRKADE 356

☐ >gi|3695088|gb|AAC62638.1| ☒ DN p63 beta [Homo sapiens]  
 gi|12024748|gb|AAG45611.1| DN p63 beta [Homo sapiens]  
 Length = 461

Score = 65.5 bits (158), Expect = 1e-09  
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
 IP D+ P F+V+ + SA W YS L+KL+ + + M P  
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRI MLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 130 V-IRAMPVYKKA EHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIVTLETR 236

Query: 297 HGTLGRKSI SVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 237 DGQVLGRRCFEARICACPRDRKADE 262



☐ >gi|13751177|emb|CAC37100.1| ☒ TA1 KET gamma protein [Rattus norvegicus]  
Length = 470

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 148 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 206

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 207 V-IRAMPVYKKAHEVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 258

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 259 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 313

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 314 DGQVLGRRCFEARICACPRDRKADE 339

☐ >gi|3695086|gb|AAC62637.1| ☒ TA p63 beta [Homo sapiens]  
Length = 516

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 126 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 184

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 185 V-IRAMPVYKKAHEVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 236

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 237 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 291

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 292 DGQVLGRRCFEARICACPRDRKADE 317

☐ >gi|3695092|gb|AAC62640.1| ☒ TA\*p63 beta [Mus musculus]  
gi|32812142|gb|AAP87983.1| p63 TA beta [Mus musculus]  
Length = 555

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRLMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 224 V-IRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 276 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 331 DGQVLGRRCFEARICACPRDRKADE 356

☐ >gi|1463021|gb|AAC37335.1| p53 [Canis familiaris]  
 Length = 281

Score = 65.5 bits (158), Expect = 1e-09  
 Identities = 46/175 (26%), Positives = 77/175 (44%), Gaps = 15/175 (8%)

Query: 152 WCYSNALEKLFVK--KKTPTFDVTYMQPSDYSRLKLRLMLVYSNSQYAYQTISRC-QDD 208  
 W YS L KLF + K PV V+ P + +R M +Y S++ + + RC +  
 Sbjct: 16 WTYSPLLNLKFCQLAKTCPVQLWVSSPPPPNTC---VRAMAIYKKSEFVTEVVRCPHHE 72

Query: 209 IAKDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVP 268  
 D + A +H++R G + +DR + P + T  
 Sbjct: 73 RCSDSSDGLAPPQHLIRV-----EGNLRKYLDDRNTFRHSVVVPYEPPEVGSDYTT- 124

Query: 269 VSLEFLCQNSC-PTMERRATTLVFTVENEHGTLGRKKSISVKICSCPGRDMEKDD 322  
 + ++C +SC M RR + T+E+ G +LGR S V++C+CP RD ++  
 Sbjct: 125 IHYNYMCNSSCMGGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPRDRRTEE 179

☐ >gi|13751181|emb|CAC37102.1| ☒ DN KET gamma protein [Rattus norvegicus]  
 Length = 393

Score = 65.1 bits (157), Expect = 2e-09  
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
 IP D+ P F+V+ + SA W YS L+KL+ + M P  
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRLMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 237 DGQVLGRRCFEARICACPRDRKADE 262

☐ >gi|3695096|gb|AAC62642.1| ☒ DN p63 gamma [Mus musculus]  
gi|32812146|gb|AAP87987.1| p63 DN gamma [Mus musculus]  
Length = 389

Score = 65.1 bits (157), Expect = 2e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P  
Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G  
Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E  
Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322  
G +LGR+ +IC+CP RD + D+  
Sbjct: 237 DGQVLGRRCFEARICACPGDRKADE 262

☐ >gi|3695098|gb|AAC62643.1| ☒ DN p63 beta [Mus musculus]  
gi|32812145|gb|AAP87986.1| p63 DN beta [Mus musculus]  
Length = 461

Score = 65.1 bits (157), Expect = 2e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P  
Sbjct: 71 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
+ +R M VY +++ + + RC + +++++ A H++R G  
Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
ED R +VLV P + + T V F+C +SC M RR ++ T+E  
Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322  
G +LGR+ +IC+CP RD + D+  
Sbjct: 237 DGQVLGRRCFEARICACPGDRKADE 262

☐ >gi|13751179|emb|CAC37101.1| ☒ TA2 KET gamma protein [Rattus norvegicus]  
Length = 487

Score = 65.1 bits (157), Expect = 2e-09  
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
IP D+ P F+V+ + SA W YS L+KL+ + + M P  
Sbjct: 165 IPSNTDYPGP-HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 224 V-IRAMPVYKKAHEHVTEVVKRCPNHELSEFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 276 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 331 DGQVLGRRCFEARICACPGRDRKADE 356

☐ >gi|12643523|sp|Q9XSK8|P73\_CERAE Tumor protein p73 (p53-like transcription factor protein)  
 gi|4803650|emb|CAA72224.1| P53-like transcription factor [Cercopithecus aethiops]  
 Length = 637

Score = 65.1 bits (157), Expect = 2e-09  
 Identities = 57/210 (27%), Positives = 94/210 (44%), Gaps = 30/210 (14%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLF--VKKKTPVTFDVTYMQPSDY 181  
 IP D+ P F V + SA W YS L+KL+ + K P+ V+ P  
 Sbjct: 115 IPSNTDYPGP-HHFEVTFQSSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSAPPPPGT 173

Query: 182 SRLKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDAS-----F 233  
 + +R M VY +++ + RC + ++ +D A H++R + S  
 Sbjct: 174 A---IRAMPVYKKAHEVTDIVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPV 230

Query: 234 TGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFT 292  
 TGR+ +V+V P + + T + F+C +SC M RR ++ T  
 Sbjct: 231 TGRQ-----SVVVPYE----PPQVGTEFTT-ILYNFMCNSSCVGGMNRRPILIIIT 276

Query: 293 VENEHGTLGRKKSISVKICSCPGRDMEKDD 322  
 +E G +LGR+S +IC+CP RD + D+  
 Sbjct: 277 LETRDGQVLGRRSFEGRICACPGRDRKADE 306

☐ >gi|3273745|gb|AAC24830.1| ☒ p53 homolog [Homo sapiens]  
 Length = 356

Score = 65.1 bits (157), Expect = 2e-09  
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183  
 IP D+ P F+V+ + SA W YS L+KL+ + + M P  
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241  
 + +R M VY +++ + + RC + +++++ A H++R G  
 Sbjct: 130 V-IRAMPVYKKAHEHVTEVVKRCPNHELSEFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296  
 ED R +VLV P + + T V F+C +SC M RR ++ T+E  
 Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322  
 G +LGR+ +IC+CP RD + D+  
 Sbjct: 237 DGQVLGRRCFEARICACPGRRDRKADE 262

☐ >gi|2842672|sp|Q64662|P53\_SPEBE Cellular tumor antigen p53 (Tumor suppressor p53)  
 gi|1165312|gb|AAA85628.1| p53  
 Length = 314

Score = 65.1 bits (157), Expect = 2e-09  
 Identities = 46/172 (26%), Positives = 75/172 (43%), Gaps = 14/172 (8%)

Query: 154 YSNALEKLFVK--KKTPTVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRCQDDIAK 211  
 YS +L KLF + K PV V P ++R M +Y SQ+ + + RC  
 Sbjct: 104 YSPSLNKLFCQLAKTCPVQLWVDSTPPPG---TRVRAMAIYKKSQHMTEVVRRCPHHERC 160

Query: 212 DGAKDFAHKEHVVRCLNPASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVPVSL 271  
 + A +H++R G + +DR + P + + T +  
 Sbjct: 161 SDSDGLAPPQHLIRV-----EGNLRAEYLDDRNTFRHSVVVPYEPPEVGSESTT-IHY 212

Query: 272 EFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPGRDMEKDD 322  
 ++C +SC M RR + T+E+ G LLGR S V++C+CP RD ++  
 Sbjct: 213 NYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRRDRRTEE 264

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Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
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 Number of letters in database: 478,769,834  
 Number of sequences in database: 1,486,004

Lambda K H  
 0.318 0.133 0.394

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 320,929,099  
 Number of Sequences: 1486004  
 Number of extensions: 13374429  
 Number of successful extensions: 24389  
 Number of sequences better than 10.0: 100  
 Number of HSP's better than 10.0 without gapping: 179  
 Number of HSP's successfully gapped in prelim test: 8  
 Number of HSP's that attempted gapping in prelim test: 24038  
 Number of HSP's gapped (non-prelim): 187  
 length of query: 338  
 length of database: 478,769,834

effective HSP length: 124  
effective length of query: 214  
effective length of database: 294,505,338  
effective search space: 63024142332  
effective search space used: 63024142332  
T: 11  
A: 40  
X1: 16 ( 7.3 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 41 (21.7 bits)  
S2: 73 (32.7 bits)

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:  
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Sch  ffer,  
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),  
"Gapped BLAST and PSI-BLAST: a new generation of protein database search  
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057859850-06894-5218

Query= SEQID32  
(7 letters)

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,477,204 sequences; 474,244,320 total letters

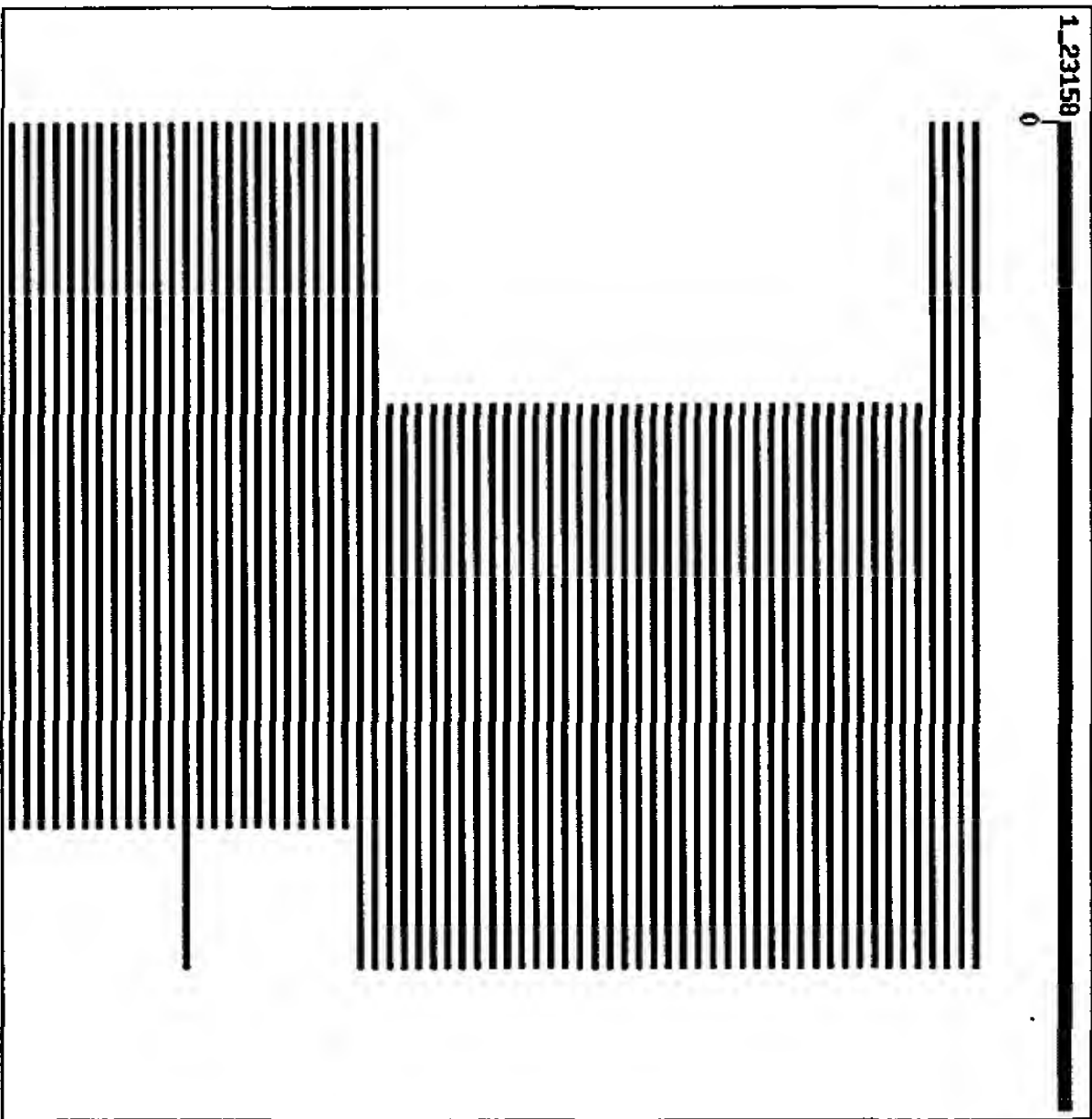
If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

[Mouse-over to show define and scores. Click to show alignments](#)

EXHIBIT E



Sequences producing significant alignments:

	Score	E
(bits)	Value	
gi 32440603 emb CAA90618.2  Hypothetical protein K09A11.5 [...]	23	468
gi 21355617 ref NP_651115.1  CG10873-PA (Drosophila melanog...	23	628
gi 25009887 gb AA71112.1  AT28346p (Drosophila melanogaster)	23	628
gi 31207283 ref XP_312608.1  ENSANGP0000014785 [Anopheles ...]	22	843
gi 27885063 gb AA026000.1  Hypothetical protein T05C3.4 [Ca...	21	2037
gi 19909128 gb AAW03124.1 AF489528.1 transforming growth fa...	21	2037
gi 9910586 ref NP_064303.1  latent transforming growth fact...	21	2037
gi 15238132 ref NP_196594.1  expressed protein (Arabidopsis...	21	2037
gi 23008906 ref ZP_00050155.1  hypothetical protein [Magnet...	21	2037
gi 17535887 ref NP_493679.1  Q/N-rich domain Prion like pro...	21	2037
gi 1890196 emb CAA70995.1  hypothetical protein [Methanosar...	21	2037
gi 21241370 ref NP_640952.1  hypothetical protein [Xanthomo...	21	2037
gi 22327352 ref NP_680337.1  expressed protein [Arabidopsis...	21	2037
gi 7506860 pir T29475 hypothetical protein T01D1.6 - Caeno...	21	2037
gi 23466945 ref ZP_00122531.1  hypothetical protein [Haemop...	21	2037
gi 20853732 ref XP_153430.1  hypothetical protein XP_153430...	21	2037
gi 15146444 gb AAK84663.1 AF351824.1 sterolin-2 [Homo sapiens]	21	2037



gi 30913084 sp Q8CG19 LTBL_MOUSE	Latent transforming growth...	21	2037	<a href="#">L</a>
gi 25990358 gb AAN76497.1 AF288451.1	LTBP-15 protein [Xenop...	21	2037	
gi 17563888 ref NP_504449.1	Putative plasma membr...	21	2037	<a href="#">L</a>
gi 14579069 gb AAK69136.1 AF280997.1	maturase K [Phyllodad...	21	2037	
gi 17535161 ref NP_496221.1	Cysteine rich repeat containin...	21	2037	<a href="#">L</a>
gi 28499491 ref XP_144125.2	similar to KIAA1337 protein (H...	21	2037	<a href="#">L</a>
gi 17564630 ref NP_506849.1	Q/N-rich domain Prion like pro...	21	2037	<a href="#">L</a>
gi 21227944 ref NP_633866.1	Sulfite reductase, assimilator...	21	2037	
gi 30913083 sp Q8CG18 LTBS_MOUSE	Latent transforming growth...	21	2037	
gi 30352201 gb AAP31860.1	glucagon-like peptide 1 receptor...	21	2037	
gi 22537398 ref NP_688249.1	site-specific recombinase, pha...	21	2037	
gi 11967971 ref NP_071882.1	sterolin 2; ATP-binding casset...	21	2037	<a href="#">L</a>
gi 23050656 ref ZP_00077526.1	hypothetical protein [Methan...	21	2037	
gi 23953861 gb AAN38831.1	latent transforming growth facto...	21	2037	<a href="#">L</a>
gi 15088540 gb AAK84078.1 AF324494.1	sterolin-2 (Homo sapiens)	21	2037	<a href="#">L</a>
gi 12483915 gb AAG53890.1 AF280604.1	latent transforming gr...	21	2037	<a href="#">L</a>
gi 7495994 pir T30136	hypothetical protein C14C11.8 - Caen...	21	2037	
gi 17557986 ref NP_504494.1	Q/N-rich domain Prion like pro...	21	2037	<a href="#">L</a>
gi 7110605 ref NP_036860.1	glucagon-like peptide 1 recepto...	21	2037	<a href="#">L</a>
gi 4557731 ref NP_000618.1	latent transforming growth fact...	21	2037	<a href="#">L</a>
gi 17567385 ref NP_510839.1	Predicted CDS, cysteine rich r...	21	2037	<a href="#">L</a>
gi 21311480 gb AAM46745.1 AF456376.1	maturase [Phyllodadus...	21	2037	<a href="#">L</a>
gi 25054368 ref XP_192826.1	latent transforming growth fac...	21	2037	<a href="#">L</a>
gi 21449820 emb CAD13505.1	latent TGR-beta binding protein...	21	2037	
gi 15227656 ref NP_181183.1	hypothetical protein [Arabidop...	21	2733	
gi 17544688 ref NP_502452.1	Putative protein family member...	20	3667	<a href="#">L</a>
gi 7493833 pir JC5808	G protein-coupled receptor 1 - yeast...	19	6602	
gi 27717643 ref XP_234914.1	similar to presenilin-like pro...	19	6602	<a href="#">L</a>
gi 26335705 dbj BAC31553.1	unnamed protein product [Mus mu...	19	6602	
gi 13474878 ref NP_106448.1	nif-specific regulatory protei...	19	6602	
gi 6320170 ref NP_010249.1	G-protein-coupled receptor at p...	19	6602	
gi 30148365 ref XP_293082.2	similar to mucin [Homo sapiens]	19	6602	<a href="#">L</a>
gi 27711652 ref XP_231993.1	similar to KRAB zinc finger pr...	19	6602	<a href="#">L</a>
gi 133241 sp P10281 HMT2_ASPOR	Ribonuclease T2 precursor (R...	19	6602	
gi 23509305 ref NP_701972.1	hypothetical protein [Plasmodi...	19	6602	
gi 19424359 gb AAL88721.1 AC114257.6	hypothetical protein [...	19	6602	
gi 7578595 gb AAF64095.1 AF207880.1	teashirt 2 [Mus musculus]	19	6602	<a href="#">L</a>
gi 22213650 emb CAC86940.1	Iron-sulfur protein (Acidilanus ...	18	11887	
gi 24266658 gb AAN52280.1 AF480620.1	phenylalanine ammonia-...	18	11887	
gi 20864524 ref XP_146397.1	similar to Putative nuclear pr...	18	11887	<a href="#">L</a>
gi 29653448 ref NP_819140.1	sulfatase [Coxiella burnetii R...	18	11887	
gi 27682355 ref XP_240891.1	hypothetical protein XP_240891...	18	11887	<a href="#">L</a>
gi 20218817 emb CAC84493.1	putative nucleoside diphosphate...	18	11887	
gi 14600950 ref NP_147476.1	hypothetical protein [Aeropyru...	18	11887	
gi 23478566 gb EAL15617.1	hypothetical protein [Plasmodium...	18	11887	
gi 25518475 pir D86295	hypothetical protein T24D18.16 - Ar...	18	11887	
gi 18860391 ref NP_569607.1	hypothetical protein [Psilotum...	18	11887	
gi 2768974 ref XP_224724.1	similar to hypothetical protei...	18	11887	<a href="#">L</a>
gi 2398707 emb CAB16172.1	intein in MCL536.28c [Mycobacte...	18	11887	
gi 16765589 ref NP_461204.1	ferredoxin-type protein: elect...	18	11887	
gi 28828206 gb AAO50887.1	hypothetical protein [Dictyostel...	18	11887	
gi 18394319 ref NP_563990.1	ovule development protein, put...	18	11887	

gi 17563034 ref NP_503423.1	Q/N-rich domain Prion like pro...	18	11887	<a href="#">L</a>
gi 15802761 ref NP_288788.1	ferredoxin-type protein: elect...	18	11887	
gi 7657283 ref NP_056623.1	keratin associated protein 5-1;...	18	11887	<a href="#">L</a>
gi 32455621 ref NP_862103.1	hypothetical protein [Streptoc...	18	11887	
gi 23041377 ref ZP_00072839.1	hypothetical protein [Tricho...	18	11887	
gi 24113594 ref NP_708104.1	ferredoxin-type protein: elect...	18	11887	
gi 30680844 ref NP_849617.1	expressed protein [Arabidopsis...	18	11887	
gi 22327896 ref NP_200493.2	F-box protein family [Arabidop...	18	11887	
gi 16123217 ref NP_406530.1	ferredoxin-type protein Napr [...	18	11887	
gi 23135090 ref ZP_00116849.1	hypothetical protein [Cytoph...	18	11887	
gi 29732192 ref XP_295569.1	hypothetical protein XP_295569...	18	11887	<a href="#">L</a>
gi 27705140 ref XP_228089.1	similar to RIKEN CDNA 1700027D...	18	11887	<a href="#">L</a>
gi 27484392 ref XP_210345.1	similar to keratin associated ...	18	11887	<a href="#">L</a>
gi 10176786 dbj BAB09900.1	gene_id:MKI9.29-pir T01344-si...	18	11887	
gi 12619768 gb AAG60534.1 AF215129.1	conotoxin scaffold III...	18	11887	
gi 26248456 ref NP_754496.1	Hypothetical protein [Escheric...	18	11887	
gi 29840062 ref NP_829168.1	conserved hypothetical protein...	18	11887	
gi 15827239 ref NP_301502.1	conserved hypothetical protein...	18	11887	
gi 2145939 pir S72760	psp1 protein - Mycobacterium leprae ...	18	11887	
gi 31242377 ref XP_321619.1	ENSANGP0000011747 [Anopheles ...	18	11887	
gi 26334265 dbj BAC30850.1	unnamed protein product [Mus mu...	18	15950	<a href="#">L</a>
gi 29827714 ref NP_822348.1	hypothetical protein [Streptom...	18	15950	
gi 28520318 ref XP_289380.1	hypothetical protein XP_289380...	18	15950	<a href="#">L</a>
gi 7488433 pir T01524	zinc finger protein homolog T10M13.2...	18	15950	
gi 29249108 gb EAA40627.1	GRP_23.41158_38234 [Giardia lamb...	18	15950	
gi 29250510 gb EAA42002.1	GRP_68_2582_684 [Giardia lamba...	18	15950	
gi 18411882 ref NP_567225.1	zinc finger protein identical ...	18	15950	
gi 7513280 pir T09539	protein ANA - human >gi 3738222 dbj ...	18	15950	<a href="#">L</a>
gi 17532455 ref NP_496495.1	Predicted CDS, putative endopl...	18	15950	<a href="#">L</a>
gi 1314734 gb AA99804.1	220 kDa silk protein	18	15950	
gi 15193021 gb AAK91661.1 AF378824.1	myeloid-specific perox...	18	15950	

Alignments

Get selected sequences      [Select all](#)      [Deselect all](#)

>gi|32440603|emb|CAA90618.2|      Hypothetical protein K09A11.5 [Caenorhabditis elegans]  
length = 650

Score = 23.1 bits (47), Expect = 468  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1      FXCQNSC 7  
                    F CQNSC  
Sbjct: 606      FTCQNSC 612

gi|21355617|ref|NP\_651115.1|      CG10873-PA [Drosophila melanogaster]  
gi|7211767|gb|AAF40427.1|AF224713.1      transcription factor p53 [Drosophila melano]  
gi|7211769|gb|AAF40428.1|AF224714.1      transcription factor p53 [Drosophila melano]  
gi|7381624|gb|AAF61572.1|AF244918.1      p53 tumor suppressor-like protein [Drosophi



gi|8272608|gb|AA074277.1|AF250918.1 transcription factor [Drosophila melanogaster]  
 gi|8453176|gb|AA075270.1|AF263722.1 transcription factor p53 [Drosophila melano  
 gi|10726710|gb|AA056087.2|CG10873-PA [Drosophila melanogaster]  
 gi|17861528|gb|AA039241.1|GH11591p [Drosophila melanogaster]  
 gi|18032162|gb|AA056639.1|AF192555.1 p53-like regulator of apoptosis and cell cyc  
 melanogaster]  
 Length = 385

Score = 22.7 bits (46), Expect = 628  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 FXCONS 7  
 F CONS  
 Sbjct: 225 FVCCONS 231

>gi|25009887|gb|AA071112.1|AT28346p [Drosophila melanogaster]  
 Length = 519

Score = 22.7 bits (46), Expect = 628  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 FXCONS 7  
 F CONS  
 Sbjct: 359 FVCCONS 365

>gi|31207283|ref|XP\_312608.1|ENSANGP00000014785 [Anopheles gambiae]  
 gi|21295812|gb|EA07957.1|ENSANGP00000014785 [Anopheles gambiae str. FST]  
 Length = 338

Score = 22.3 bits (45), Expect = 843  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 FXCONS 7  
 F CONS  
 Sbjct: 273 FLCCONS 279

>gi|27885063|gb|AA026000.1|Hypothetical protein T05C3.4 [Caenorhabditis elegans]  
 Length = 431

Score = 21.0 bits (42), Expect = 2037  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONS 7  
 CONS  
 Sbjct: 5 CONS 9

>gi|19909128|gb|AA03124.1|AF489528.1 transforming growth factor-beta binding  
 Length = 1394

Score = 21.0 bits (42), Expect = 2037  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONS 7  
 CONS  
 Sbjct: 44 CONS 48

>gi|9910586|ref|NP\_064303.1|latent transforming growth factor beta binding p  
 TGF beta binding protein [Mus musculus]  
 gi|3493176|gb|AAC33307.1|latent TGF beta binding protein [Mus musculus]  
 Length = 1713

Score = 21.0 bits (42), Expect = 2037  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONS 7  
 CONS  
 Sbjct: 362 CONS 366

>gi|15238132|ref|NP\_196594.1|expressed protein [Arabidopsis thaliana]  
 gi|11291567|ref|T50820|hypothetical protein F18D22.90 - Arabidopsis thaliana  
 gi|8953413|emb|CAB96688.1|putative protein [Arabidopsis thaliana]  
 Length = 369

Score = 21.0 bits (42), Expect = 2037  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONS 7  
 CONS  
 Sbjct: 96 CONS 100

>gi|23008906|ref|ZP\_00050155.1|hypothetical protein [Magnetospirillum magnetot  
 Length = 294

Score = 21.0 bits (42), Expect = 2037  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONS 7  
 CONS  
 Sbjct: 114 CONS 118

>gi|17535887|ref|NP\_493679.1|Q/N-rich domain Prion like protein PGN-61 (pgn-  
 elegans)  
 gi|14574221|gb|AA037887.2|Activated in blocked unfolded protein response protein  
 [Caenorhabditis elegans]  
 Length = 395

Score = 21.0 bits (42), Expect = 2037  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 202 CONSC 206

>gi|1890196|emb|CAA70995.1| hypothetical protein [Methanosarcina barkeri]  
Length = 225

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 139 CONSC 143

>gi|21241370|ref|NP\_640952.1| hypothetical protein [Xanthomonas axonopodis pv. c  
gi|21106700|gb|AA035488.1| Xanthomonas axonopodis pv. citri  
Length = 167

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 127 CONSC 131

>gi|22327352|ref|NP\_680337.1| expressed protein [Arabidopsis thaliana]  
Length = 128

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 27 CONSC 31

>gi|7506860|pir|T29475 hypothetical protein T01D1.6 - Caenorhabditis elegans  
Length = 411

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 218 CONSC 222

>gi|23466945|ref|ZP\_00122531.1| hypothetical protein [Haemophilus somnus 129PT]  
Length = 343

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 255 CONSC 259

>gi|20853732|ref|XP\_153430.1| hypothetical protein XP\_153430 [Mus musculus]  
Length = 98

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 80 CONSC 84

>gi|15146444|gb|AA084663.1|AF351824.1 sterolin-2 [Homo sapiens]  
Length = 672

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 80 CONSC 84

>gi|30913084|sp|Q8CG19|LTBL\_MOUSE Latent transforming growth factor beta binding  
precursor (LTBP-1) (Transforming growth factor beta-1  
binding protein 1) (TGF-beta1-BP-1)  
gi|26006334|gb|AA077250.1| latent transforming growth factor beta binding prote  
musculus]  
Length = 1713

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 362 CONSC 366

>gi|25990358|gb|AA076497.1|AF288451.1 LTBP-1S protein [Xenopus laevis]  
Length = 1398

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7  
CONSC  
Sbjct: 44 CONSC 48

☐ >gi|17563888|ref|NP\_504449.1| **L** putative plasma membrane protein family  
at least 6 transmembrane domains, nematode specific  
[Caenorhabditis elegans]  
gi|7507180|pir|T31732 hypothetical protein T05C3.4 - Caenorhabditis elegans  
Length = 779  
Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)  
Query: 3 CQNSC 7  
CQNSC  
Sbjct: 5 CQNSC 9

☐ >gi|14579069|gb|AAK69136.1|AF280997.1 maturase K [Phyllostachys alpinus]  
Length = 511  
Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)  
Query: 3 CQNSC 7  
CQNSC  
Sbjct: 183 CQNSC 187

☐ >gi|17535161|ref|NP\_496221.1| **L** Cysteine rich repeat containing protein [Caenor]  
gi|7505943|pir|T23682 hypothetical protein M02G9.3 - Caenorhabditis elegans  
gi|3878599|emb|CAB04626.1| Hypothetical protein M02G9.3 [Caenorhabditis elegans]  
Length = 294  
Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)  
Query: 3 CQNSC 7  
CQNSC  
Sbjct: 176 CQNSC 180

☐ >gi|28499491|ref|XP\_144125.2| **L** similar to KIAA1337 protein [Homo sapiens] [Mus]  
Length = 1357  
Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)  
Query: 3 CQNSC 7  
CQNSC  
Sbjct: 582 CQNSC 586

☐ >gi|17564630|ref|NP\_506849.1| **L** Q/N-rich domain Prion like protein PQN-71 (pqn-  
elegans)

gi|7508303|pir|T25169 hypothetical protein T23F1.6 - Caenorhabditis elegans  
gi|3880082|emb|CAB03405.1| C. elegans PQN-71 protein (corresponding sequence T23F  
[Caenorhabditis elegans]  
Length = 330  
Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)  
Query: 3 CQNSC 7  
CQNSC  
Sbjct: 235 CQNSC 239

☐ >gi|21227944|ref|NP\_633866.1| sulfite reductase, assimilatory-type [Methanosarc]  
gi|20906367|gb|AAM31538.1| Sulfite reductase, assimilatory-type [Methanosarcina m  
Length = 224  
Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)  
Query: 3 CQNSC 7  
CQNSC  
Sbjct: 138 CQNSC 142

☐ >gi|30913083|sp|Q8CG18|LTBS\_MOUSE Latent transforming growth factor beta binding  
1S precursor (LTBP-1) (Transforming growth factor  
beta-1 binding protein 1) (TGF-beta1-BP-1)  
gi|26006335|gb|AAN77251.1| latent transforming growth factor beta binding protein  
musculus]  
Length = 1389  
Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)  
Query: 3 CQNSC 7  
CQNSC  
Sbjct: 39 CQNSC 43

☐ >gi|30352201|gb|AAP31860.1| glucagon-like peptide 1 receptor|GLP-1 receptor [Rat]  
Length = 463  
Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)  
Query: 3 CQNSC 7  
CQNSC  
Sbjct: 458 CQNSC 462

☐ >gi|22537398|ref|NP\_688249.1| site-specific recombinase, phage integrase family  
agalactiae 2603V/R] **3** site-specific recombinase, phage integrase f  
gi|22534273|gb|AAN00122.1|AE014249 **3**  
agalactiae 2603V/R]

Length = 399

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 391 CQNSC 395

>gi|11967971|ref|NP\_071882.1| **L** sterolin 2; ATP-binding cassette, subfamily G,  $\alpha$  sapiens]  
gi|17432916|sp|Q9H221|ABG8\_HUMAN **L** ATP-binding cassette, sub-family G, member 8 (  
gi|11692802|gb|AAG40004.1|AF320294.1 **L** ABCG8 [Homo sapiens]  
Length = 673

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 80 CQNSC 84

>gi|23050656|ref|ZP\_00077526.1| hypothetical protein [Methanosarcina barkeri]  
Length = 228

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 142 CQNSC 146

>gi|23953861|gb|AA38831.1| **L** latent transforming growth factor beta binding protein [musculus]  
Length = 55

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 25 CQNSC 29

>gi|15088540|gb|AA84078.1|AF324494.1 **L** sterolin-2 [Homo sapiens]  
Length = 673

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7

CQNSC  
Sbjct: 80 CQNSC 84

>gi|12483915|gb|AAG53890.1|AF280604.1 **L** latent transforming growth factor beta 1 precursor [Mus musculus]  
Length = 165

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 44 CQNSC 48

>gi|7495994|dic|T30136 hypothetical protein C14C11.8 - Caenorhabditis elegans  
Length = 654

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 556 CQNSC 560

>gi|17557986|ref|NP\_504494.1| **L** Q/N-rich domain Prion like protein PQN-13 (70.0 [Caenorhabditis elegans]  
gi|14573802|gb|AA96110.2| Prion-like-(q/n-rich)-domain-bearing protein 1 [Caenorhabditis elegans]  
Length = 661

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 563 CQNSC 567

>gi|7110605|ref|NP\_036860.1| **L** glucagon-like peptide 1 receptor; Pancreatic beta-2 the glucocorticoid hormone glucagon-like peptide 1 [Rattus norvegicus]  
gi|417070|sp|P32301|GLP1\_RAT glucagon-like peptide 1 receptor precursor (GLP-1 receptor) (GLP-1-R) (GLP-1R)  
gi|423852|pir|A46172 glucagon-like peptide 1 receptor - rat  
gi|387868|gb|AA73377.1| **L** [Rat mRNA sequence], gene product  
Length = 463

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7

CQNSC  
Sbjct: 458 CQNSC 462

>gi|4557731|ref|NP\_000618.1| **L** latent transforming growth factor beta binding p  
precursor [Homo sapiens]  
gi|135691|sp|P22064|LTBS\_HUMAN latent transforming growth factor beta binding pro  
IS precursor (LTBP-1) (Transforming growth factor  
beta-1 binding protein 1) (TGF-beta1-BP-1)  
gi|107945|pir||A35626 transforming growth factor beta-1-binding protein - human  
gi|339548|gb|AA61160.1| **L** transforming growth factor-beta 1 binding protein prec  
length = 1394

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 44 CQNSC 48

>gi|17567385|ref|NP\_510839.1| **L** predicted CDS, cysteine rich repeat containing p  
member [Caenorhabditis elegans]  
gi|7500204|pir||T29699 hypothetical protein F31A3.1 - Caenorhabditis elegans  
gi|1326321|gb|AAB36856.1| Hypothetical protein F31A3.1 [Caenorhabditis elegans]  
length = 242

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 117 CQNSC 121

>gi|21311480|gb|AAM46745.1|AF456376\_1 maturase [Phyllocladus trichomanoides]  
length = 511

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 183 CQNSC 187

>gi|25054368|ref|XP\_192826.1| **L** latent transforming growth factor beta binding p  
musculus]  
length = 1520

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7

CQNSC  
Sbjct: 169 CQNSC 173

>gi|21449820|emb|CAD13505.1| latent TGF-beta binding protein 1 [Xenopus laevis]  
length = 1399

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CQNSC 7  
CQNSC  
Sbjct: 44 CQNSC 48

>gi|15227656|ref|NP\_181183.1| hypothetical protein [Arabidopsis thaliana]  
gi|25408473|pir||E84780 hypothetical protein At2g36420 [imported] - Arabidopsis t  
gi|4581142|gb|AAD24626.1| unknown protein [Arabidopsis thaliana]  
length = 439

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 1 FXCQNSC 7  
F C+NSC  
Sbjct: 57 FSCENSC 63

>gi|17544688|ref|NP\_502452.1| **L** Putative protein family member, nematode specifi  
elegans]  
gi|7511394|pir||T28079 hypothetical protein ZK896.1 - Caenorhabditis elegans  
gi|3881865|emb|CAB05322.1| Hypothetical protein ZK896.1 [Caenorhabditis elegans]  
length = 410

Score = 20.2 bits (40), Expect = 3667  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCQNSC 7  
F C NSC  
Sbjct: 187 FTCHNSC 193

>gi|7493833|pir||JC5808 G protein-coupled receptor 1 - yeast (Saccharomyces cere  
length = 962

Score = 19.3 bits (38), Expect = 6602  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCQNS 6  
F CQNS  
Sbjct: 458 FSCQNS 463

>gi|27717643|ref|XP\_234914.1| similar to presenilin-like protein 1 [Homo sapiens]
norvegicus]
Length = 1759

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
CONS
Sbjct: 859 FSCONS 864

>gi|26335705|dbj|BAC31553.1| unnamed protein product [Mus musculus]
gi|28913719|gb|AAH48570.1| Similar to protein tyrosine phosphatase, receptor type
polypeptide 2 [Mus musculus]
Length = 118

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
CONS
Sbjct: 108 FSCONS 113

>gi|13474878|ref|NP\_106448.1| nif-specific regulatory protein, nifA [Mesorhizobium
gi|14025634|dbj|BAB52234.1| nif-specific regulatory protein; NifA [Mesorhizobium]
Length = 583

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
CONS
Sbjct: 466 FACONS 471

>gi|6320170|ref|NP\_010249.1| G-protein-coupled receptor at plasma membrane; int
two-hybrid system with Gpa2p; Gpr1p [Saccharomyces
cerevisiae]
gi|26394417|sp|Q12361|GPR1\_YEAST G protein-coupled receptor GPR1
gi|2132416|pir|S67568 probable membrane protein YDL035c - yeast (Saccharomyces
cerevisiae)
gi|1279681|emb|CAA96454.1| unknown [Saccharomyces cerevisiae]
gi|1431015|emb|CAA98593.1| ORF YDL035c [Saccharomyces cerevisiae]
Length = 961

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
CONS
Sbjct: 457 FSCONS 462

>gi|30148365|ref|XP\_293082.2| similar to mucin [Homo sapiens]
norvegicus]
Length = 1293

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
CONS
Sbjct: 917 FSCONS 922

>gi|27711652|ref|XP\_231993.1| similar to KRAB zinc finger protein 6D [Mus musc
norvegicus]
Length = 303

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
CONS
Sbjct: 99 FSCONS 104

Get selected sequences Selected all Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Jul 10, 2003 1:49 AM
Number of letters in database: 474,244,320
Number of sequences in database: 1,477,204

Lambda K H
0.362 0.277 2.25
Gapped
Lambda K H
0.294 0.110 0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 3,712,852
Number of Sequences: 1477204
Number of extensions: 5677
Number of successful extensions: 129
Number of sequences better than 20000.0: 100
Number of HSP's better than 20000.0 without gapping: 129
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 129
length of query: 7
length of database: 474,244,320
effective HSP length: 0
effective length of query: 9

effective length of database: 474,244,320  
effective search space: 4268198880  
effective search space used: 4268198880

T: 11

A: 40

X1: 14 ( 7.3 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 35 (20.1 bits)

S2: 35 (18.0 bits)

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RTD: 1057861440-028425-7091

Query= SEQID23 (9 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF 1,477,204 sequences; 474,244,320 total letters

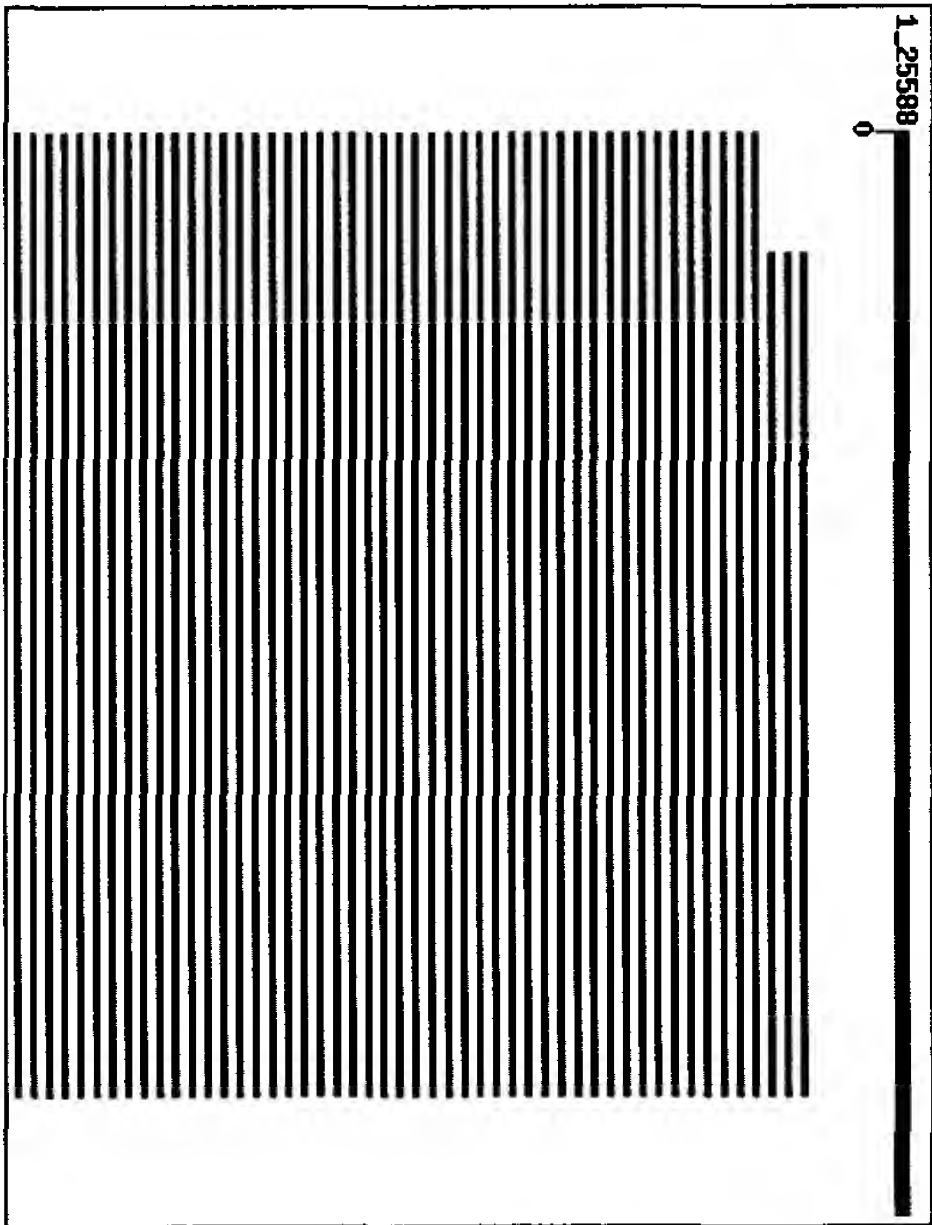
If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

EXHIBIT F



Sequences producing significant alignments:

	Score (bits)	E Value
gi 31207283 ref XP_312608.1  ENSANGP00000014785 [Anopheles ...]	31	2.4
gi 21355617 ref NP_651115.1  CG10873-PA [Drosophila melanog...]	28	14
gi 25009887 gb AAW71112.1  AT28346p [Drosophila melanogaster]	28	14
gi 3695096 gb AAC62642.1  DN p63 gamma [Mus musculus]	26	80
gi 13751181 emb CAC37102.1  DN KET gamma protein [Rattus no...]	26	80
gi 13751173 emb CAC37098.1  TA1 KET alpha protein [Rattus n...]	26	80
gi 20428532 gb AAK81886.1  DN p73 gamma [Homo sapiens]	26	80
gi 1813455 gb AAH41833.1  p53	26	80
gi 19909983 dbj BAB87245.1  deltan p73 beta [Homo sapiens] ...	26	80
gi 7248451 gb AAF43492.1  p51 isoform delnbeta [Homo sapiens]	26	80
gi 20892181 ref XP_147232.1  transformation related protein...	26	80
gi 3695094 gb AAC62641.1  TA*p63 alpha [Mus musculus]	26	80
gi 12060406 dbj BAB20591.1  delta N p73L [Homo sapiens]	26	80
gi 4803651 emb CAA72225.1  p73 splice variant [Cercopithec...	26	80
gi 13751179 emb CAC37101.1  TA2 KET gamma protein [Rattus n...]	26	80
gi 15072750 emb CAC48053.1  p63 delta [Homo sapiens]	26	80
gi 29470179 gb AAO74632.1  p73 [Danio rerio]	26	80
gi 2581764 gb AAB82420.1  p53 [Cricketulus griseus]	26	80
gi 8217484 emb CAB92742.1  dj1092A11.2 (tumor protein p73) ...	26	80
gi 2370178 emb CAA72221.1  second splice variant [Homo sapi...]	26	80
gi 21264484 sp P79820 P53_ORYLA Cellular tumor antigen p53 ...	26	80
gi 1184759 gb AAA87577.1  p53 tumor suppressor homolog	26	80
gi 1184757 gb AAA87576.1  p53 tumor suppressor homolog	26	80
gi 7248450 gb AAF43491.1  p51 isoform delnalpha [Homo sapiens]	26	80



gi 7248447 gb AAFA43488.1	p51 isoform TA63beta [Homo sapiens]	26	80	
gi 3273745 gb AAC24830.1	p53 homolog [Homo sapiens]	26	80	<b>L</b>
gi 473579 gb AAB41344.1	tumor suppressor p53 [Mesocricetus ...]	26	80	
gi 2752178 emb CAD10682.1	p53 protein [Monodelphis domestica]	26	80	
gi 12024746 gb AAG45609.1	TA p63 gamma [Homo sapiens]	26	80	
gi 3695098 gb AAC62643.1	DN p63 beta [Mus musculus]	26	80	<b>L</b>
gi 4689086 gb AAD27752.1	AF043641.1 p73 [Barbus barbus]	26	80	
gi 6755883 ref NP_035771.1	transformation related protein ...	26	80	<b>L</b>
gi 1244762 gb AAA98563.1	p53 tumor suppressor homolog	26	80	
gi 13751187 emb CAC37105.1	DN KRT beta protein [Rattus nor...	26	80	<b>L</b>
gi 13751175 emb CAC37099.1	DN KRT alpha protein [Rattus no...	26	80	<b>L</b>
gi 23308709 ref NP_694518.1	deltap63 isoform alpha 1; tum...	26	80	<b>L</b>
gi 26339452 gb BAC33397.1	unnamed protein product [Mus mu...	26	80	<b>L</b>
gi 23308711 ref NP_694519.1	deltap63 isoform gamma; tumor...	26	80	<b>L</b>
gi 3695082 gb AAC62635.1	TA p63 alpha [Homo sapiens]	26	80	<b>L</b>
gi 1698502 gb AAC60146.1	p53 [Oryzias latipes] >gi 1208249...	26	80	
gi 20850793 ref XP_131858.1	transformation related protein...	26	80	<b>L</b>
gi 13195250 gb AAK16622.1	AF314148.1 p63 DNA binding protei...	26	80	<b>L</b>
gi 3510328 gb BAA32592.1	p51A [Homo sapiens] >gi 3695078 ...	26	80	<b>L</b>
gi 13751185 emb CAC37104.1	TA1 KRT beta protein [Rattus no...	26	80	<b>L</b>
gi 451931 gb AAA37086.1	tumor suppressor protein [Mesocric...	26	80	
gi 1813453 gb AAB41832.1	p53	26	80	<b>L</b>
gi 3695080 gb AAC62634.1	DN p63 gamma [Homo sapiens] >gi 7...	26	80	<b>L</b>
gi 1813451 gb AAB41831.1	p53	26	80	<b>L</b>
gi 3970717 emb CAA76562.1	KRT protein [Homo sapiens]	26	80	<b>L</b>
gi 23308685 ref NP_689454.1	deltap63 isoform alpha 2; tum...	26	80	<b>L</b>
gi 3445484 gb BAA32433.1	p73H [Homo sapiens]	26	80	<b>L</b>
gi 7689271 gb AAF67733.1	AF253323.1 p53 tumor suppressor-1...	26	80	<b>L</b>
gi 17985367 gb AAL50211.1	tumor protein [Canis familiaris]	26	80	<b>L</b>
gi 31543818 ref NP_003713.3	tumor protein p73-like; tumor ...	26	80	<b>L</b>
gi 19909981 gb BAB87244.1	deltan p73 alpha [Homo sapiens]...	26	80	<b>L</b>
gi 4101546 gb AAD01196.1	tumor suppressor protein p53 [Ory...	26	80	
gi 1813457 gb AAB41834.1	p53	26	80	<b>L</b>
gi 1244764 gb AAA98564.1	p53 tumor suppressor homolog	26	80	<b>L</b>
gi 7440008 gb JG6176	tumor suppressor protein p53 - Chine...	26	80	<b>L</b>
gi 12856636 gb BAA30732.1	unnamed protein product [Mus mu...	26	80	<b>L</b>
gi 19850152 gb AAL99584.1	AF285104.1 p53-like transcription...	26	80	<b>L</b>
gi 7320915 emb CAB81954.1	p73 delta-N protein [Mus musculus]	26	80	<b>L</b>
gi 129370 sp Q00366 P53_MESAU	Cellular tumor antigen p53 (T...	26	80	
gi 7689273 gb AAF67734.1	AF253324.1 p73-like protein [Mya a...	26	80	<b>L</b>
gi 3695088 gb AAC62638.1	DN p63 beta [Homo sapiens] >gi 12...	26	80	<b>L</b>
gi 2370177 emb CAA72219.1	first splice variant [Homo sapiens]	26	80	<b>L</b>
gi 3510330 gb BAA32593.1	p51B [Homo sapiens] >gi 7248446 ...	26	80	<b>L</b>
gi 1890327 emb CAA70109.1	p53 tumour suppressor [Cricketul...	26	80	
gi 7248452 gb AAF43493.1	p51 isoform delndelta [Homo sapiens]	26	80	<b>L</b>
gi 12060487 gb BAB20631.1	DN p63 alpha [Gallus gallus]	26	80	<b>L</b>
gi 3695092 gb AAC62640.1	TA*p63 beta [Mus musculus]	26	80	<b>L</b>
gi 10720194 sp Q9TNA1 P53_TUPGB	Cellular tumor antigen p53 ...	26	80	
gi 7248448 gb AAF43489.1	p51 isoform TA63delta [Homo sapi...	26	80	<b>L</b>
gi 3695090 gb AAC62639.1	TA*p63 gamma [Mus musculus]	26	80	<b>L</b>
gi 2499428 sp Q09185 P53_CRIGR	Cellular tumor antigen p53 (...)	26	80	
gi 12643523 sp Q9XSR8 P73_CERAE	Tumor protein p73 (p53-like...	26	80	

gi 4885645 ref NP_005418.1	tumor protein p73; p53-related ...	26	80	<b>L</b>
gi 12024745 gb AAG45608.1	TA p63 beta [Homo sapiens]	26	80	
gi 9507209 ref NP_062094.1	transformation related protein ...	26	80	<b>L</b>
gi 3695086 gb AAC62637.1	TA p63 beta [Homo sapiens]	26	80	<b>L</b>
gi 4887145 gb AAD32213.1	p73 [Mus musculus]	26	80	<b>L</b>
gi 13751183 emb CAC37103.1	TA2 KRT beta protein [Rattus no...	26	80	<b>L</b>
gi 3644040 gb AAC43038.1	CUSP [Homo sapiens] >gi 3695084 g...	26	80	<b>L</b>
gi 13751177 emb CAC37100.1	TA1 KRT gamma protein [Rattus n...	26	80	<b>L</b>
gi 23867780 gb BAC21014.1	claudin4L2 [Xenopus laevis]	25	144	<b>L</b>
gi 17859712 ref NP_506256.1	Cadherin protein like [Caenorh...	24	194	<b>L</b>
gi 27705398 ref XP_230942.1	similar to dJ551D2.1.1 (Cadher...	24	194	<b>L</b>
gi 28071273 gb BAC55966.1	tumor necrosis factor receptor...	24	194	
gi 21623719 gb BAC00941.1	HT-protein [Lycopersicon peruvi...	24	260	
gi 17227039 gb AAL37982.1	AF442140.1 style-specific self-in...	24	260	
gi 21623726 gb BAC00944.1	HT-A protein [Lycopersicon chmi...	24	260	
gi 23113187 ref ZP_00098587.1	hypothenical protein [Desulf...	24	260	
gi 30039744 ref NP_835472.1	rolling circle replication pro...	24	260	
gi 21623723 gb BAC00943.1	HT-protein [Lycopersicon parvif...	24	260	
gi 21623729 gb BAC00945.1	HT-A protein [Lycopersicon hirs...	24	260	
gi 17227037 gb AAL37981.1	AF442139.1 style-specific self-in...	24	260	
gi 15218576 ref NP_174690.1	expressed protein [Arabidopsis...	24	349	
gi 129372 sp P10361 P53_RAT	Cellular tumor antigen p53 (Tum...	23	468	<b>L</b>
gi 7259331 gb BAA922786.1	p53 [Macaca fuscata]	23	468	
gi 693787 gb AAB31269.1	tumor suppressor [Canis familiaris]	23	468	

## Alignments

## Get selected sequences

Select all

Deselect all

>gi|31207283|ref|XP\_312608.1| ENSANGP00000014785 [Anopheles gambiae]  
gi|21295812|gb|BAA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PEEST]  
Length = 338

Score = 30.8 bits (65), Expect = 2.4  
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 ICSCPRD 9

ICSCPRD ICSCPRD

Sbjct: 310 ICSCPRD 317

>gi|21355617|ref|NP\_651115.1| CG10873-PA [Drosophila melanogaster]  
gi|7211767|gb|AAF40427.1| AF224713.1 transcription factor p53 [Drosophila melano]  
gi|7211769|gb|AAF40428.1| AF224714.1 transcription factor p53 [Drosophila melano]  
gi|7381624|gb|AAF61572.1| AF244918.1 p53 tumor suppressor-like protein [Drosophi]  
gi|8272608|gb|AAF74277.1| AF250918.1 transcription factor [Drosophila melanogast]  
gi|8453176|gb|AAF5270.1| AF263722.1 transcription factor p53 [Drosophila melano]  
gi|10726710|gb|AAF56087.2| CG10873-PA [Drosophila melanogaster]  
gi|17861528|gb|AAL39241.1| GH11591P [Drosophila melanogaster]

gi|18032162|gb|AA156639.1|AF192555.1 p53-like regulator of apoptosis and cell cyc  
melanogaster]  
Length = 385

Score = 28.2 bits (59), Expect = 14  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 ICSCPKRD 9  
IC+CPKRD  
Sbjct: 260 ICTCPKRD 267

>gi|25009887|gb|AA171112.1| AT28346p (Drosophila melanogaster)  
Length = 519

Score = 28.2 bits (59), Expect = 14  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 ICSCPKRD 9  
IC+CPKRD  
Sbjct: 394 ICTCPKRD 401

>gi|3695096|gb|AAC62642.1| L DN p63 gamma (Mus musculus)  
Length = 389

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9  
RIC+CP RD  
Sbjct: 249 RICACPKRD 257

>gi|13751181|emb|CAC37102.1| L DN KET gamma protein (Rattus norvegicus)  
Length = 393

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9  
RIC+CP RD  
Sbjct: 249 RICACPKRD 257

>gi|13751173|emb|CAC37098.1| L TAI KET alpha protein (Rattus norvegicus)  
Length = 663

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9  
RIC+CP RD  
Sbjct: 326 RICACPKRD 334

>gi|20428532|gb|AAK81886.1| L DN p73 gamma (Homo sapiens)  
Length = 426

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9  
RIC+CP RD  
Sbjct: 244 RICACPKRD 252

>gi|1813455|gb|AAB41833.1| p53  
Length = 238

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9  
RIC+CP RD  
Sbjct: 166 RICACPKRD 174

>gi|19909983|dbj|BAB87245.1| L deltan p73 beta (Homo sapiens)  
gi|20428530|gb|AAK81885.1| L DN p73 beta (Homo sapiens)  
Length = 450

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9  
RIC+CP RD  
Sbjct: 244 RICACPKRD 252

>gi|7248451|gb|AAF43492.1| p51 isoform delNPbeta (Homo sapiens)  
Length = 461

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9  
RIC+CP RD  
Sbjct: 249 RICACPKRD 257

>gi|20892181|ref|XP\_147232.1| L transformation related protein 63 (Mus musculus)  
Length = 465

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9

RIC+CP RD  
Sbjct: 128 RICACPGRD 136

>gi|3695094|gb|AAC62641.1| TA\*p63 alpha [Mus musculus]  
Length = 680

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 343 RICACPGRD 351

>gi|12060406|db|BAB20591.1| delta N p73L [Homo sapiens]  
Length = 501

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 164 RICACPGRD 172

>gi|4803651|emb|CAA72225.1| p73 splice variant [Cercopithecus aethiops]  
Length = 499

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 293 RICACPGRD 301

>gi|13751179|emb|CAC37101.1| TA2 KET gamma protein [Rattus norvegicus]  
Length = 487

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 343 RICACPGRD 351

>gi|15072750|emb|CAC48053.1| p63 delta [Homo sapiens]  
Length = 232

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 191 RICACPGRD 199

>gi|29470179|gb|AA074632.1| p73 [Danio rerio]  
Length = 640

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 300 RICACPGRD 308

>gi|2581764|gb|AA82420.1| p53 [Cricetulus griseus]  
Length = 205

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 148 RICACPGRD 156

>gi|8217484|emb|CAB92742.1| dJ1092A11.2 (tumor protein p73) [Homo sapiens]  
Length = 661

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 318 RICACPGRD 326

>gi|2370178|emb|CAA72221.1| second splice variant [Homo sapiens]  
Length = 588

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPFRD 9  
RIC+CP RD  
Sbjct: 245 RICACPGRD 253

>gi|21264484|sp|P79820|P53\_ORYLA Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|4101544|gb|AA01195.1| tumor suppressor protein p53 [Oryzias latipes]  
Length = 352

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 254 RICACPRD 262

>gi|1184759|gb|AA87577.1| p53 tumor suppressor homolog  
Length = 189

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 89 RICACPRD 97

>gi|1184757|gb|AA87576.1| p53 tumor suppressor homolog  
Length = 228

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 97 RICACPRD 105

>gi|7248450|gb|AA43491.1| p51 isoform delnalpna [Homo sapiens]  
Length = 586

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 249 RICACPRD 257

>gi|7248447|gb|AA43488.1| p51 isoform TAP63beta [Homo sapiens]  
Length = 516

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 304 RICACPRD 312

>gi|3273745|gb|AAC24830.1| p53 homolog [Homo sapiens]  
Length = 356

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 249 RICACPRD 257

>gi|473579|gb|AA81344.1| tumor suppressor p53 [Mesocricetus auratus]  
Length = 396

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 276 RICACPRD 284

>gi|27527178|emb|CAD10682.1| p53 protein [Monodelphis domestica]  
Length = 258

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 145 RICACPRD 153

>gi|12024746|gb|AA645609.1| TA p63 gamma [Homo sapiens]  
Length = 487

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 343 RICACPRD 351

>gi|3695098|gb|AAC62643.1| DN p63 beta [Mus musculus]  
Length = 461

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCCKRD 9  
RIC+CP RD  
Sbjct: 249 RICACPRD 257

>gi|4689086|gb|AAD27752.1|AF043641.1 p73 [Barbus barbuis]  
Length = 641

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 301 RICACPGRD 309

>gi|6755883|ref|NP\_035771.1| L transformation related protein 63; KET protein; i  
[Mus musculus]  
gi|3445482|dbj|BA32432.1| L p73H [Mus musculus]  
gi|3695100|gb|AAC62644.1| L DN p63 alpha [Mus musculus]  
Length = 586

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 249 RICACPGRD 257

>gi|1244762|gb|AA98563.1| p53 tumor suppressor homolog  
Length = 564

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 298 RICACPGRD 306

>gi|13751187|emb|CAC37105.1| L DN KET beta protein [Rattus norvegicus]  
Length = 461

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 249 RICACPGRD 257

>gi|13751175|emb|CAC37099.1| L DN KET alpha protein [Rattus norvegicus]  
Length = 586

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 249 RICACPGRD 257

>gi|23308709|ref|NP\_694518.1| L deltaMp63 isoform alpha 1; tumor protein p63 [D:  
gi|22652331|gb|AA03690.1|AF412283.1 L DN p63 alpha 1 [Danio rerio]  
Length = 588

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 247 RICACPGRD 255

>gi|26339452|dbj|BAC33397.1| unnamed protein product [Mus musculus]  
Length = 284

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 249 RICACPGRD 257

>gi|23308712|ref|NP\_694519.1| L deltaMp63 isoform gamma; tumor protein p63 [Dani  
gi|22652335|gb|AA03692.1|AF412285.1 L DN p63 gamma [Danio rerio]  
Length = 457

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 247 RICACPGRD 255

>gi|3695082|gb|AAC62635.1| L TA p63 alpha [Homo sapiens]  
Length = 641

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 304 RICACPGRD 312

>gi|1698502|gb|AAC60146.1| p53 [Oryzias latipes]

gi|12082495|gb|AAC48557.1|AF212997\_1 p53 tumor suppressor [Oryzias latipes]  
Length = 351

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 253 RICACPGRD 261

>gi|20850793|ref|XP\_131858.1| L transformation related protein 73 [Mus musculus]  
gi|30794514|ref|NP\_035772.1| L transformation related protein 73 [Mus musculus]  
gi|15209244|emb|CAB81953.1| L P73 alpha protein [Mus musculus]  
Length = 631

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 285 RICACPGRD 293

>gi|13195250|gb|AAK15622.1|AF314148\_1 p63 DNA binding protein [Xenopus laevis]  
Length = 365

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 249 RICACPGRD 257

>gi|3510328|dbj|BAA32592.1| L p51A [Homo sapiens]  
gi|3695078|gb|AAC62633.1| L TA p63 gamma [Homo sapiens]  
gi|7248445|gb|AAF43486.1| p51 isoform TAp63gamma [Homo sapiens]  
Length = 448

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 304 RICACPGRD 312

>gi|13751185|emb|CAC37104.1| L TAI KER beta protein [Rattus norvegicus]  
Length = 538

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 326 RICACPGRD 334

>gi|451931|gb|AAA37086.1| tumor suppressor protein [Mesocricetus auratus]  
Length = 206

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 148 RICACPGRD 156

>gi|1813453|gb|AAB41832.1| p53  
Length = 286

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 166 RICACPGRD 174

>gi|3695080|gb|AAC62634.1| L DN p63 gamma [Homo sapiens]  
gi|7248449|gb|AAF43490.1| p51 isoform delNgamma [Homo sapiens]  
gi|12024749|gb|AAG45612.1| DN p63 gamma [Homo sapiens]  
Length = 393

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 249 RICACPGRD 257

>gi|1813451|gb|AAB41831.1| p53  
Length = 378

Score = 25.7 bits (53), Expect = 80  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
RIC+CP RD  
Sbjct: 258 RICACPGRD 266

>gi|3970717|emb|CAA76562.1| L KER protein [Homo sapiens]  
Length = 680

Score = 25.7 bits (53), Expect = 80  
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
 RIC+CP RD  
 Sbjct: 343 RICACPGRD 351

>gi|23308685|ref|NP\_689454.1| deltanp63 isoform alpha 2; tumor protein p63 [D  
 gi|21326973|gb|AA048108.1|AF487944.1 deltan p63 alpha [Danio rerio]  
 gi|22652333|gb|AA03691.1|AF412284.1 DN p63 alpha 2 [Danio rerio]  
 Length = 576

Score = 25.7 bits (53), Expect = 80  
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPGRD 9  
 RIC+CP RD  
 Sbjct: 247 RICACPGRD 255

Get selected sequences Select all Deselect all

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Jul 10, 2003 1:49 AM  
 Number of letters in database: 474,244,320  
 Number of sequences in database: 1,477,204

Lambda K H  
 0.355 0.291 2.09

Gapped  
 Lambda K H  
 0.294 0.110 0.610

Matrix: PAM30  
 Gap Penalties: Existence: 9, Extension: 1  
 Number of Hits to DB: 7,787,423  
 Number of Sequences: 1477204  
 Number of extensions: 37039  
 Number of successful extensions: 1121  
 Number of sequences better than 20000.0: 100  
 Number of HSP's better than 20000.0 without gapping: 1073  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 1121  
 length of query: 9  
 length of database: 474,244,320  
 effective HSP length: 0  
 effective length of query: 9  
 effective length of database: 474,244,320

effective search space: 4268198880  
 effective search space used: 4268198880  
 T: 11  
 A: 40  
 X1: 14 ( 7.2 bits)  
 X2: 35 (14.8 bits)  
 X3: 58 (24.6 bits)  
 S1: 35 (19.7 bits)  
 S2: 35 (18.0 bits)



NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:  
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,  
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),  
"Gapped BLAST and PSI-BLAST: a new generation of protein database search  
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057861369-027523-7419

Query= SEQID24  
(9 letters)

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,477,204 sequences; 474,244,320 total letters

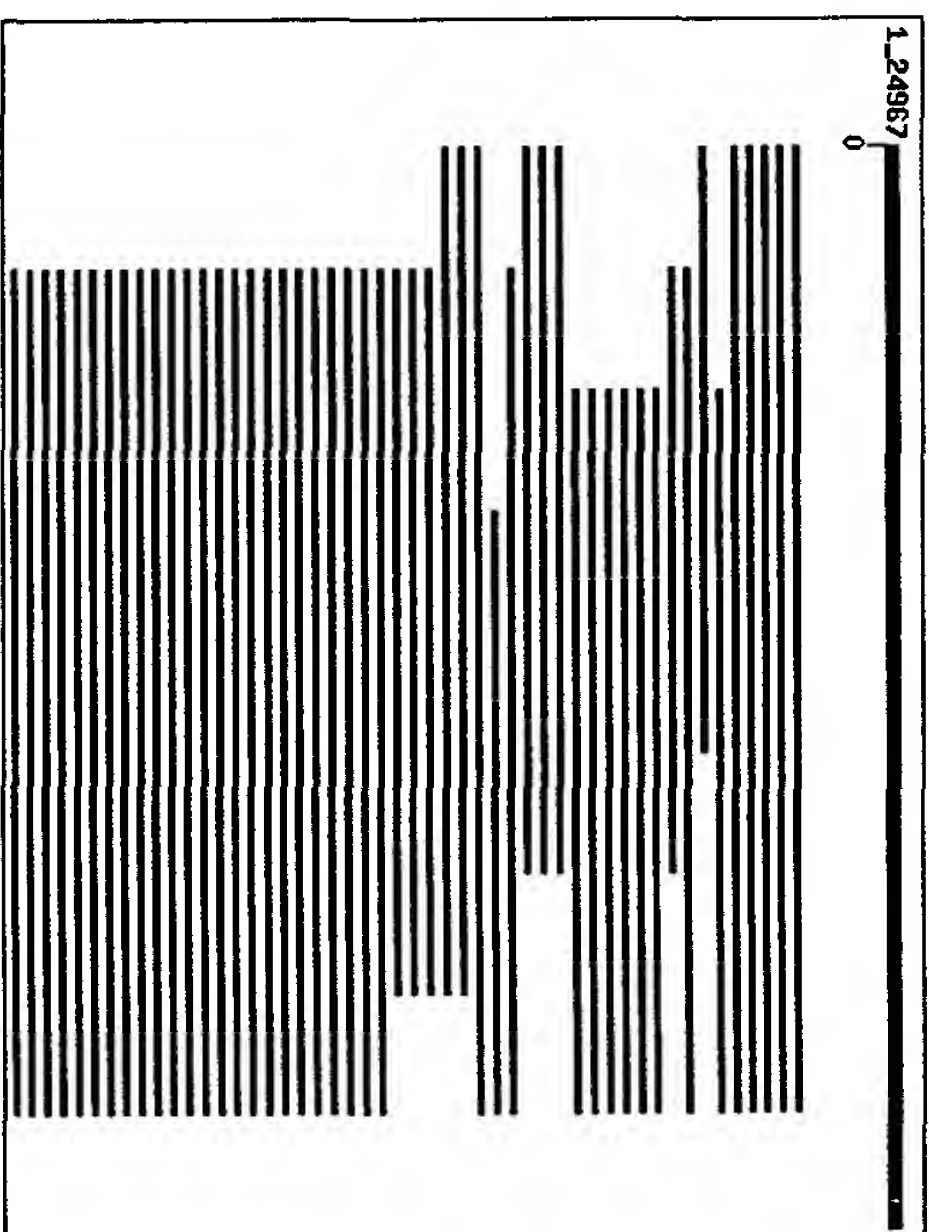
If you have any problems or questions with the results of this search  
please refer to the [BLAST page](#)

[Taxonomy reports](#)

Distribution of 113 Blast Hits on the Query Sequence

[Mouse-over to show define and scores. Click to show alignments](#)

EXHIBIT G



Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi 31207283 ref XP_312608.1  ENSANGP00000014785 [Anopheles ...]	34	0.30
gi 21355617 ref NP_651115.1  CG10873-PA [Drosophila melanog...]	31	1.8
gi 25009887 gb AAW71112.1  AT28346p [Drosophila melanogaster]	31	1.8
gi 1673504 emb CAA66181.1  G protein-coupled receptor kinas...	26	60
gi 12621084 ref NP_075217.1  G protein-coupled receptor kin...	26	60
gi 23867780 dbj BAC21014.1  claudin4L2 [Xenopus laevis]	25	144
gi 21623719 dbj BAC00941.1  HT-protein [Lycopersicon peruv...	24	260
gi 17227039 gb AAU37982.1 AF442140.1 style-specific self-in...	24	260
gi 21623726 dbj BAC00944.1  HT-A protein [Lycopersicon chm...	24	260
gi 23113187 ref ZP_00098587.1  hypothetical protein [Desulf...	24	260
gi 30039744 ref NP_835472.1  rolling circle replication pro...	24	260
gi 29565659 ref NP_817241.1  ORF82 [Pinus koraiensis] >gi 2...	24	260
gi 21623723 dbj BAC00943.1  HT-A protein [Lycopersicon parvif...	24	260
gi 21623729 dbj BAC00945.1  HT-A protein [Lycopersicon hirs...	24	260
gi 17227037 gb AAU37981.1 AF442139.1 style-specific self-in...	24	260
gi 17554334 ref NP_498645.1  Musc1e Positioning 4, transmem...	24	349
gi 14579227 gb AAK69172.1 AF289202.1 transmembrane matrix r...	24	349
gi 25395876 pir P88508 protein H1A12.6 [imported] - Caeno...	24	349
gi 15218576 ref NP_174690.1  expressed protein [Arabidopsis...	24	349
gi 15236812 ref NP_194396.1  expressed protein [Arabidopsis...	23	468
gi 17862926 gb AAU39940.1  SD03546p [Drosophila melanogaster]	23	628
gi 18150104 dbj BAB83667.1  insulin receptor [Paralichthys ...]	23	628
gi 24582874 ref NP_609236.2  CG13096-PA [Drosophila melanog...	23	628
gi 32408903 ref XP_324932.1  predicted protein [Neurospora ...]	23	628

gi 2826739 gb AAC41250.1	chordin [Gallus gallus]	23	628	<a href="#">L</a>
gi 28574699 ref NP_787974.1	CG33196-PB [Drosophila melanog...]	23	628	<a href="#">L</a>
gi 3695096 gb AAC62642.1	DN p63 gamma [Mus musculus]	22	843	<a href="#">L</a>
gi 13751181 emb CAC37102.1	DN KET gamma protein [Rattus no...]	22	843	<a href="#">L</a>
gi 13751173 emb CAC37098.1	TA1 KET alpha protein [Rattus n...]	22	843	<a href="#">L</a>
gi 20428532 gb AAK81886.1	DN p73 gamma [Homo sapiens]	22	843	<a href="#">L</a>
gi 1813455 gb AAB41833.1	p53	22	843	<a href="#">L</a>
gi 19909983 dbj BAB87245.1	deltan p73 beta [Homo sapiens] ...	22	843	<a href="#">L</a>
gi 7248451 gb AAF43492.1	p51 isoform delnbeta [Homo sapiens]	22	843	<a href="#">L</a>
gi 20892181 ref XP_147232.1	transformation related protein...	22	843	<a href="#">L</a>
gi 3695094 gb AAC62641.1	TA*p63 alpha [Mus musculus]	22	843	<a href="#">L</a>
gi 12060406 dbj BAB20591.1	delta N p73L [Homo sapiens]	22	843	<a href="#">L</a>
gi 4803651 emb CAA72225.1	p73 splice variant [Cercopithec...	22	843	<a href="#">L</a>
gi 13751179 emb CAC37101.1	TA2 KET gamma protein [Rattus n...]	22	843	<a href="#">L</a>
gi 15072750 emb CAC48053.1	p53 delta [Homo sapiens]	22	843	<a href="#">L</a>
gi 29470179 gb AAO74632.1	p73 [Dario rerio]	22	843	<a href="#">L</a>
gi 2581764 gb AAB82420.1	p53 [Cricetus griseus]	22	843	<a href="#">L</a>
gi 8217484 emb CAB92742.1	du1092A11.2 (tumor protein p73) ...	22	843	<a href="#">L</a>
gi 2370178 emb CAA72221.1	second splice variant [Homo sapi...]	22	843	<a href="#">L</a>
gi 21264484 sp P79820 P53_ORYLA	Cellular tumor antigen p53 ...	22	843	<a href="#">L</a>
gi 1184757 gb AAA87577.1	p53 tumor suppressor homolog	22	843	<a href="#">L</a>
gi 1184757 gb AAA87576.1	p53 tumor suppressor homolog	22	843	<a href="#">L</a>
gi 7248450 gb AAF43491.1	p51 isoform delNalpha [Homo sapiens]	22	843	<a href="#">L</a>
gi 7248447 gb AAF43488.1	p51 isoform TAP3beta [Homo sapiens]	22	843	<a href="#">L</a>
gi 3273745 gb AAC24830.1	p53 homolog [Homo sapiens]	22	843	<a href="#">L</a>
gi 473579 gb AAB41344.1	tumor suppressor p53 [Mesocricetus ...]	22	843	<a href="#">L</a>
gi 27527178 emb CAD10682.1	p53 protein [Monodelphis domest...]	22	843	<a href="#">L</a>
gi 12024746 gb AAG45609.1	TA p63 gamma [Homo sapiens]	22	843	<a href="#">L</a>
gi 3695098 gb AAC62643.1	DN p63 beta [Mus musculus]	22	843	<a href="#">L</a>
gi 4689086 gb AAD27752.1 AF043641	p73 [Barbus barbus]	22	843	<a href="#">L</a>
gi 6755883 ref NP_035771.1	transformation related protein ...	22	843	<a href="#">L</a>
gi 1244762 gb AAA98563.1	p53 tumor suppressor homolog	22	843	<a href="#">L</a>
gi 13751187 emb CAC37105.1	DN KET beta protein [Rattus nor...]	22	843	<a href="#">L</a>
gi 13751175 emb CAC37099.1	DN KET alpha protein [Rattus no...]	22	843	<a href="#">L</a>
gi 23308709 ref NP_694518.1	deltanp63 isoform alpha 1; tum...	22	843	<a href="#">L</a>
gi 26339452 dbj BAC33397.1	unnamed protein product [Mus mu...]	22	843	<a href="#">L</a>
gi 23308711 ref NP_694519.1	deltanp63 isoform gamma; tumor...	22	843	<a href="#">L</a>
gi 3695082 gb AAC62635.1	TA p63 alpha [Homo sapiens]	22	843	<a href="#">L</a>
gi 1698502 gb AAC60146.1	p53 [Oryzias latipes] >gi 1208249...	22	843	<a href="#">L</a>
gi 20850793 ref XP_131858.1	transformation related protein...	22	843	<a href="#">L</a>
gi 13195250 gb AAK15622.1 AF314148	p63 DNA binding protei...	22	843	<a href="#">L</a>
gi 3510328 dbj BAA32592.1	p51A [Homo sapiens] >gi 3695078 ...	22	843	<a href="#">L</a>
gi 13751185 emb CAC37104.1	TA1 KET beta protein [Rattus no...]	22	843	<a href="#">L</a>
gi 451931 gb AAA37086.1	tumor suppressor protein [Mesocrice...]	22	843	<a href="#">L</a>
gi 1813453 gb AAB41832.1	p53	22	843	<a href="#">L</a>
gi 3695080 gb AAC62634.1	DN p63 gamma [Homo sapiens] >gi 7...	22	843	<a href="#">L</a>
gi 1813451 gb AAB41831.1	p53	22	843	<a href="#">L</a>
gi 3970717 emb CAA76562.1	KET protein [Homo sapiens]	22	843	<a href="#">L</a>
gi 23308685 ref NP_689454.1	deltanp63 isoform alpha 2; tum...	22	843	<a href="#">L</a>
gi 3445484 dbj BAA32433.1	p73H [Homo sapiens]	22	843	<a href="#">L</a>
gi 7689271 gb AAF67733.1 AF253323	p53 tumor suppressor-li...	22	843	<a href="#">L</a>
gi 17985367 gb AAL50211.1	tumor protein [Canis familiaris]	22	843	<a href="#">L</a>

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

gi 31543818 ref NP_003713.3	tumor protein p73-like; tumor ...	22	843	<a href="#">L</a>
gi 19909981 dbj BAB87244.1	deltan p73 alpha [Homo sapiens]...	22	843	<a href="#">L</a>
gi 4101546 gb AAD01196.1	tumor suppressor protein p53 [Ory...]	22	843	<a href="#">L</a>
gi 1813457 gb AAB41834.1	p53	22	843	<a href="#">L</a>
gi 1244764 gb AA98564.1	p53 tumor suppressor homolog	22	843	<a href="#">L</a>
gi 7440008 pir JC6176	tumor suppressor protein p53 - Chine...	22	843	<a href="#">L</a>
gi 1285636 dbj BAB30732.1	unnamed protein product [Mus mu...]	22	843	<a href="#">L</a>
gi 19850152 gb AAL99584.1 AF285104	p53-like transcription...	22	843	<a href="#">L</a>
gi 7320915 emb CAB81954.1	p73 delta-N protein [Mus musculus]	22	843	<a href="#">L</a>
gi 129370 sp Q00366 P53_MESAU	Cellular tumor antigen p53 (T...	22	843	<a href="#">L</a>
gi 7689273 gb AAF67734.1 AF253324	p73-like protein [Mya a...	22	843	<a href="#">L</a>
gi 3695088 gb AAC62638.1	DN p63 beta [Homo sapiens] >gi 12...	22	843	<a href="#">L</a>
gi 2370177 emb CAA72219.1	first splice variant [Homo sapiens]	22	843	<a href="#">L</a>
gi 3510330 dbj BAA32593.1	p51B [Homo sapiens] >gi 7248446 ...	22	843	<a href="#">L</a>
gi 1890327 emb CAA70109.1	p53 tumour suppressor [Cricetulu...]	22	843	<a href="#">L</a>
gi 7248452 gb AAF43493.1	p51 isoform delNdelta [Homo sapiens]	22	843	<a href="#">L</a>
gi 12060487 dbj BAB20631.1	DN p63 alpha [Gallus gallus]	22	843	<a href="#">L</a>
gi 3695092 gb AAC62640.1	TA*p63 beta [Mus musculus]	22	843	<a href="#">L</a>
gi 10720194 sp Q9Y7A1 P53_TUPEB	Cellular tumor antigen p53 ...	22	843	<a href="#">L</a>
gi 7248448 gb AAF43489.1	p51 isoform TAP3delta [Homo sapi...]	22	843	<a href="#">L</a>
gi 3695090 gb AAC62639.1	TA*p63 gamma [Mus musculus]	22	843	<a href="#">L</a>
gi 2499428 sp O09185 P53_CRIGR	Cellular tumor antigen p53 (...]	22	843	<a href="#">L</a>
gi 12643523 sp Q9XSR8 P73_CERAE	Tumor protein p73 (p53-like...	22	843	<a href="#">L</a>
gi 4885645 ref NP_005418.1	tumor protein p73; p53-related ...	22	843	<a href="#">L</a>

#### Alignments

Get selected sequences

Select all

Deselect all

>gi|31207283|ref|XP\_312608.1| ENSANGP00000014785 [Anopheles gambiae]  
gi|21295812|gb|EAA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PRST]

Length = 338

Score = 33.7 bits (72), Expect = 0.30

Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 KICSCPXR 9

KICSCPXR

Subject: 309 KICSCPXR 317

>gi|21355617|ref|NP\_651115.1| CG10873-PA [Drosophila melanogaster]

gi|7211767|gb|AAF40427.1|AF224713.1 transcription factor p53 [Drosophila melano

gi|7211769|gb|AAF40428.1|AF224714.1 transcription factor p53 [Drosophila melano

gi|7381624|gb|AAF61572.1|AF244918.1 p53 tumor suppressor-like protein [Drosophi

gi|8272608|gb|AAF74277.1|AF250918.1 transcription factor [Drosophila melanogast

gi|8453176|gb|AAF75270.1|AF263722.1 transcription factor p53 [Drosophila melano

gi|10726710|gb|AAF56087.2| CG10873-PA [Drosophila melanogaster]

gi|17861528|gb|AAL39241.1| GH11591P [Drosophila melanogaster]

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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gi|18032162|gb|AAJ56639.1|AF192555.1 p53-like regulator of apoptosis and cell cys  
melanogaster]  
Length = 385

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KICSCPARD 9  
KIC+CPKRD  
Sbjct: 259 KICTCPKRD 267

>gi|25009887|gb|AAJ71112.1| AT28346p [Drosophila melanogaster]  
Length = 519

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KICSCPARD 9  
KIC+CPKRD  
Sbjct: 393 KICTCPKRD 401

>gi|1673504|emb|CAA66181.1| G protein-coupled receptor kinase GRK4B [Rattus n  
Length = 544

Score = 26.1 bits (54), Expect = 60  
Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

Query: 1 KICSC---PKRD 9  
KICSC PKR+  
Sbjct: 508 KICSCILRPKRN 519

>gi|12621084|ref|NP\_075217.1| G protein-coupled receptor kinase 2, groucho ger  
norvegicus]  
gi|1673503|emb|CAA66180.1| G protein-coupled receptor kinase GRK4A [Rattus norv  
Length = 575

Score = 26.1 bits (54), Expect = 60  
Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

Query: 1 KICSC---PKRD 9  
KICSC PKR+  
Sbjct: 539 KICSCILRPKRN 550

>gi|23867780|dbj|BAC21014.1| claudin4L2 [Xenopus laevis]  
Length = 213

Score = 24.8 bits (51), Expect = 144  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPARD 9

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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CSCPXR+  
Sbjct: 183 CSCPXR 189

>gi|21623719|dbj|BAC00941.1| HT-protein [Lycopersicon peruvianum]  
Length = 96

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPARD 9  
CSCP+D  
Sbjct: 61 CSCPARD 67

>gi|17227039|gb|AAJ37982.1|AF442140.1 style-specific self-incompatibility putat  
HT-A2 [Solanum chacoense]  
Length = 77

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPARD 9  
CSCP+D  
Sbjct: 44 CSCPARD 50

>gi|21623726|dbj|BAC00944.1| HT-A protein [Lycopersicon chmielewskii]  
Length = 89

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPARD 9  
CSCP+D  
Sbjct: 55 CSCPARD 61

>gi|23113187|ref|ZP\_00098587.1| hypothetical protein [Desulfitobacterium hafnien  
Length = 590

Score = 24.0 bits (49), Expect = 260  
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 2 ICS-CPKRD 9  
IC+ CPKRD  
Sbjct: 78 ICNCPKRD 86

>gi|30039744|ref|NP\_835472.1| rolling circle replication protein [Vibrio cholera  
gi|29888081|gb|AAO93096.1| rolling circle replication protein [Vibrio cholerae ph  
Length = 359

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICSCPK 7  
ICSCPK  
Sbjct: 80 ICSCPK 85

>gi|29565659|ref|NP\_817241.1| ORF82 [Pinus koraiensis]  
gi|29469758|gb|AA074086.1| ORF82 [Pinus koraiensis]  
Length = 82

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 1 KICSCP 6  
KICSCP  
Sbjct: 19 KICSCP 24

>gi|21623723|dbj|BAC00943.1| HT-Protein [Lycopersicon parviflorum]  
Length = 90

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9  
CSCPK+D  
Sbjct: 55 CSCPKRD 61

>gi|21623729|dbj|BAC00945.1| HT-A protein [Lycopersicon hirsutum]  
Length = 84

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9  
CSCPK+D  
Sbjct: 50 CSCPKRD 56

>gi|17227037|gb|AAU37981.1|AF442139.1 style-specific self-incompatibility putative  
HT-A1 [Solanum chacoense]  
Length = 99

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9  
CSCPK+D  
Sbjct: 66 CSCPKRD 72

>gi|17554334|ref|NP\_498645.1| L Muscle Positioning 4, transmembrane matrix receptor  
embryonic muscle attachment and epithelial cell adhesion  
at hemidesmosomes (230.1 kD) (mup-4) [Caenorhabditis  
elegans]

gi|15789306|gb|AAA28092.5| Muscle positioning protein 4 [Caenorhabditis elegans]  
Length = 2104

Score = 23.5 bits (48), Expect = 349  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KICGCPK 7  
KIC CPK  
Sbjct: 1476 KICGCPK 1482

>gi|14579227|gb|AAK69172.1|AF289202.1 L transmembrane matrix receptor MUP-4 [Caenorhabditis elegans]  
Length = 2104

Score = 23.5 bits (48), Expect = 349  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KICGCPK 7  
KIC CPK  
Sbjct: 1476 KICGCPK 1482

>gi|25395876|pic|F88508 protein H14A12.6 (imported) - Caenorhabditis elegans  
Length = 794

Score = 23.5 bits (48), Expect = 349  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KICGCPK 7  
KIC CPK  
Sbjct: 144 KICGCPK 150

>gi|15218576|ref|NP\_174690.1| expressed protein [Arabidopsis thaliana]  
gi|25518170|pic|B86467 hypothetical protein F23M19.5 - Arabidopsis thaliana  
gi|5091617|gb|AAD39605.1|AC007454.4 Contains similarity to gi|479356 protein kinase  
is a member of the PF100954 S-locus glycoprotein family  
and contains a PF100069 Eukaryotic protein kinase  
domain. [Arabidopsis thaliana]

gi|19699084|gb|AAI90909.1| Atig34300/F23M19.5 [Arabidopsis thaliana]  
gi|24111429|gb|AAK46865.1| Atig34300/F23M19.5 [Arabidopsis thaliana]  
Length = 829

Score = 23.5 bits (48), Expect = 349  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9  
ICSCP R+  
Sbjct: 288 ICSCPKRD 295

[>gi|15236812|ref|NP\_194396.1| expressed protein [Arabidopsis thaliana]  
gi|7487040|pir|T08932| hypothetical protein T15N24.110 - Arabidopsis thaliana  
gi|4938504|emb|CAB43862.1| putative protein [Arabidopsis thaliana]  
gi|7269518|emb|CAB79521.1| putative protein [Arabidopsis thaliana]  
Length = 806

Score = 23.1 bits (47), Expect = 468  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 4 SCPKRD 9  
SCPKRD  
Sbjct: 184 SCPKRD 189

[>gi|17862926|gb|AL39940.1| L SD03546p [Drosophila melanogaster]  
Length = 681

Score = 22.7 bits (46), Expect = 628  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 KICSCPKR 8  
KI SCPKR  
Sbjct: 311 KIPSCPKR 318

[>gi|18150104|dbj|BAB83667.1| insulin receptor [Paralichthys olivaceus]  
Length = 1369

Score = 22.7 bits (46), Expect = 628  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 1 KICSCPKRD 9  
K+C+CPK D  
Sbjct: 705 KVCACPKRD 713

[>gi|24582874|ref|NP\_609236.2| L CG13096-PA [Drosophila melanogaster]  
gi|7297428|gb|AF52687.1| L CG13096-PA [Drosophila melanogaster]  
Length = 681

Score = 22.7 bits (46), Expect = 628  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 KICSCPKR 8  
KI SCPKR  
Sbjct: 311 KIPSCPKR 318

[>gi|32408903|ref|XP\_324932.1| predicted protein [Neurospora crassa]  
gi|28925918|gb|EAA34913.1| predicted protein [Neurospora crassa]  
Length = 229

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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Query: 2 ICSCPKR 8  
ICSCP R  
Sbjct: 134 ICSCPSR 140

[>gi|2826739|gb|AAC41250.1| chordin [gallus gallus]  
Length = 940

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICSCPKR 8  
ICSC KR  
Sbjct: 716 ICSCQKR 722

[>gi|28574699|ref|NP\_787974.1| L CG33196-PB [Drosophila melanogaster]  
gi|28380266|gb|MAN10358.2|AE003576.45 L CG33196-PB [Drosophila melanogaster]  
Length = 23054

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 ICSCPKR 8  
ICSCP+R  
Sbjct: 21341 ICSCPER 21347

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
ICSCP  
Sbjct: 20821 ICSCP 20825

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
ICSCP  
Sbjct: 17656 ICSCP 17660

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
ICSCP  
Sbjct: 16586 ICSCP 16590

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
ICSCP  
Sbjct: 12381 ICSCP 12385

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
ICSCP  
Sbjct: 10780 ICSCP 10784

Score = 21.0 bits (42), Expect = 2037  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
ICSCP  
Sbjct: 9815 ICSCP 9819

Score = 18.5 bits (36), Expect = 11887  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
+CSCP  
Sbjct: 21018 VCSCP 21022

Score = 18.5 bits (36), Expect = 11887  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
+CSCP  
Sbjct: 20927 VCSCP 20931

Score = 18.5 bits (36), Expect = 11887  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
IC+CP  
Sbjct: 11743 ICTCP 11747

Score = 18.5 bits (36), Expect = 11887  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 2 ICSCPK 7  
IC CPK  
Sbjct: 8799 ICYCPK 8804

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 18.5 bits (36), Expect = 11887  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
IC+CP  
Sbjct: 3933 ICTCP 3937

Score = 18.5 bits (36), Expect = 11887  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
IC+CP  
Sbjct: 2479 ICTCP 2483

Score = 18.5 bits (36), Expect = 11887  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6  
+CSCP  
Sbjct: 1979 VCSCP 1983

[gi|3695096|gb|AAC62642.1](#) **L** DN p63 gamma [Mus musculus]  
Length = 389

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9  
IC+CP RD  
Sbjct: 250 ICACPKRD 257

[gi|13751181|emb|CAC37102.1](#) **L** DN KET gamma protein [Rattus norvegicus]  
Length = 393

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9  
IC+CP RD  
Sbjct: 250 ICACPKRD 257

[gi|13751173|emb|CAC37098.1](#) **L** TAI KET alpha protein [Rattus norvegicus]  
Length = 663

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003



Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 327 ICACPRD 334

>gi|20428532|gb|AAK81886.1| DN p73 gamma [Homo sapiens]  
Length = 426

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 245 ICACPRD 252

>gi|1813455|gb|AAB41833.1| p53  
Length = 238

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 167 ICACPRD 174

>gi|19909983|dbj|BAB87245.1| deltan p73 beta [Homo sapiens]  
gi|20428530|gb|AAK81885.1| DN p73 beta [Homo sapiens]  
Length = 450

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 245 ICACPRD 252

>gi|7248451|gb|AAF43492.1| p51 isoform delnbeta [Homo sapiens]  
Length = 461

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 250 ICACPRD 257

>gi|20892181|ref|XP\_147232.1| transformation related protein 63 [Mus musculus]  
Length = 465

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 129 ICACPRD 136

>gi|3695094|gb|AAC62641.1| TA\*p63 alpha [Mus musculus]  
Length = 680

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 344 ICACPRD 351

>gi|12060406|dbj|BAB20591.1| delta N p73L [Homo sapiens]  
Length = 501

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 165 ICACPRD 172

>gi|4803651|emb|CAA72225.1| P73 splice variant [Cercopithecus aethiops]  
Length = 499

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 294 ICACPRD 301

>gi|13751179|emb|CAC37101.1| TA2 KET gamma protein [Rattus norvegicus]  
Length = 487

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPFRD 9  
IC+CP RD  
Sbjct: 344 ICACPRD 351



gi|15072750|emb|CAC48053.1| p63 delta [Homo sapiens]

Length = 232

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 192 ICACPGRD 199

gi|29470179|gb|AA074632.1| p73 [Danio rerio]  
Length = 640

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 301 ICACPGRD 308

gi|2581764|gb|AA82420.1| p53 [Criceetus griseus]  
Length = 205

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 149 ICACPGRD 156

gi|8217484|emb|CAB92742.1| dt1092A11.2 (tumor protein p73) [Homo sapiens]  
Length = 661

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 319 ICACPGRD 326

gi|2370178|emb|CAA72221.1| second splice variant [Homo sapiens]  
Length = 588

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 246 ICACPGRD 253

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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gi|21264484|ap|P79820|p53\_ORYLA Cellular tumor antigen p53 (Tumor suppressor p53 [Oryzias latipes])  
gi|4101544|gb|AAD01195.1| tumor suppressor protein p53 [Oryzias latipes]  
Length = 352

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 255 ICACPGRD 262

gi|1184759|gb|AA87577.1| p53 tumor suppressor homolog  
Length = 189

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 90 ICACPGRD 97

gi|1184757|gb|AA87576.1| p53 tumor suppressor homolog  
Length = 228

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 98 ICACPGRD 105

gi|7248450|gb|AAF43491.1| p51 isoform delNalpha [Homo sapiens]  
Length = 586

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

IC+CP RD

Sbjct: 250 ICACPGRD 257

gi|7248447|gb|AAF43488.1| p51 isoform TAP63beta [Homo sapiens]  
Length = 516

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

IC+CP RD  
Sbjct: 305 ICACPRGD 312

>gi|3273745|gb|AAC24830.1| p53 homolog [Homo sapiens]  
Length = 356

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9  
IC+CP RD  
Sbjct: 250 ICACPRGD 257

>gi|473579|gb|AAB41344.1| tumor supressor p53 [Mesocricetus auratus]  
Length = 396

Score = 22.3 bits (45), Expect = 843  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9  
IC+CP RD  
Sbjct: 277 ICACPRGD 284

Get selected sequences Selected all Deselect all

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
Posted date: Jul 10, 2003 1:49 AM  
Number of letters in database: 474,244,320  
Number of sequences in database: 1,477,204

Lambda K H  
0.358 0.291 2.08

Gapped  
Lambda K H  
0.294 0.110 0.610

Matrix: PAM30  
Gap Penalties: Existence: 9, Extension: 1  
Number of Hits to DB: 8,062,146  
Number of Sequences: 1477204  
Number of extensions: 39018  
Number of successful extensions: 1058  
Number of sequences better than 20000.0: 100  
Number of HSP's better than 20000.0 without gapping: 1001  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1058

length of query: 9  
length of database: 474,244,320  
effective HSP length: 0  
effective length of query: 9  
effective length of database: 474,244,320  
effective search space: 4268198880  
effective search space used: 4268198880  
T: 11  
A: 40  
X1: 14 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 35 (19.9 bits)  
S2: 35 (18.0 bits)

EXHIBIT H

NCBI

results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057861590-0767-27408

Query= SEQID25  
(9 letters)

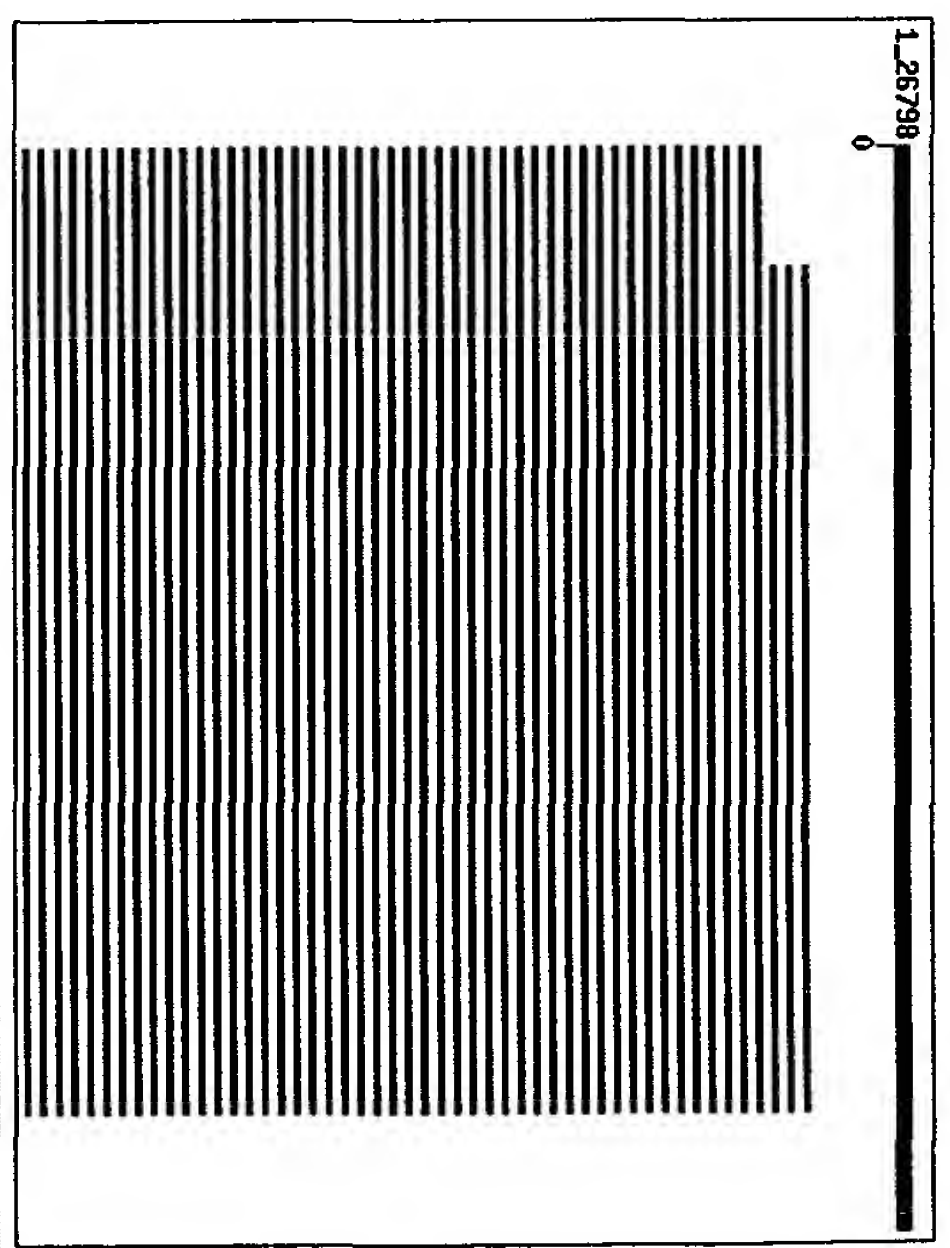
Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PIR  
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:

	Score	E
(bits)	Value	
gi 31207283 ref XP_312608.1  ENSANGP0000014785 [Anopheles ...	28	14
gi 21355617 ref NP_651115.1  CG10873-PA [Drosophila melanog...	26	80
gi 25009887 gb AAV71112.1  AT28346p [Drosophila melanogaster]	26	80
gi 129372 sp P10361 P53_RAT Cellular tumor antigen p53 (Tum...	25	108
gi 7259331 dbj BA92786.1  p53 [Macaca fuscata]	25	108
gi 693787 gb BAB31269.1  tumor suppressor [Canis familiaris]	25	108
gi 8400738 ref NP_000537.2  tumor protein p53 [Homo sapiens...	25	108
gi 4959058 gb AAD34216.1 AF071574.1 tumor suppressor protei...	25	108
gi 1709531 sp P51664 P53_SHEEP Cellular tumor antigen p53 (...	25	108
gi 129369 sp P04637 P53_HUMAN Cellular tumor antigen p53 (T...	25	108
gi 1836145 gb AAB46899.1  sequence-specific transcription f...	25	108
gi 11321107 gb AAC34052.1  p53 tumor suppressor [Rattus nor...	25	108
gi 16266760 dbj BAB69969.1  p53 [Meriones unguiculatus]	25	108
gi 21730310 pdb 1GZH C chain C, Crystal Structure Of the Br...	25	108
gi 6755881 ref NP_035770.1  transformation related protein ...	25	108
gi 200201 gb AAA39882.1  p53	25	108
gi 1154648 emb CAA62905.1  p53 [Equus caballus]	25	108
gi 2811079 sp O12946 P53_PLAIE Cellular tumor antigen p53 (...	25	108
gi 1171969 sp P41685 P53_FELCA Cellular tumor antigen p53 (...	25	108
gi 1000577 gb AAB42022.1  p53 [Canis familiaris]	25	108
gi 975651 emb CAA62450.1  p53 [Callionymus lyra]	25	108
gi 20900490 ref XP_128695.1  similar to transformation rela...	25	108
gi 8698976 gb AAF78535.1 AF223795.1 tumor suppressor p53 [On...	25	108

gi 1729419 dbj BAA08629.1	p53 gene product [Bos primigenius]	25	108	
gi 4731632 gb AAD28535.1 AF135121.1	tumor suppressor protei...	25	108	<b>L</b>
gi 10720195 sp Q9W678 P53_BARBU	Cellular tumor antigen p53 ...	25	108	
gi 223827 ref 1001197A	antigen p53, tumor	25	108	
gi 11342599 emb CAC17147.1	transformation related protein ...	25	108	<b>L</b>
gi 18859503 ref NP_571402.1	tumor protein p53; tumor suppr...	25	108	<b>L</b>
gi 10720186 sp Q9TUB2 P53_PIG	Cellular tumor antigen p53 (T...	25	108	
gi 2829194 gb AAC26190.1	tumor suppressor ortholog [Xiphop...	25	108	
gi 4996230 dbj BAA78379.1	p53 [Canis familiaris]	25	108	
gi 13591878 ref NP_112251.1	tumor protein p53; tumor prote...	25	108	<b>L</b>
gi 129374 sp P07193 P53_XENLA	Cellular tumor antigen p53 (T...	25	108	
gi 506453 emb CAA42635.1	p53 transformation suppressor [Ho...	25	108	<b>L</b>
gi 5353744 gb AAD42225.1	p53 protein [Canis familiaris]	25	108	
gi 1389675 gb AAB18936.1	tumor-suppressor [Equus caballus]	25	108	
gi 2961247 gb AAC05704.1	tumor suppressor p53 [Mus musculus]	25	108	<b>L</b>
gi 15375072 gb AAK94783.1	transformation related protein 5...	25	108	<b>L</b>
gi 8698972 gb AAF78533.1 AF23793.1	tumor suppressor p53 [On...	25	108	
gi 28975327 gb AAO60156.1	tumor suppressor p53; p53as [Mus...	25	108	<b>L</b>
gi 4959056 gb AAD34215.1 AF071573.1	tumor suppressor protei...	25	108	
gi 6841071 gb AAF28891.1 AF124298.1	p53 protein [Sus scrofa]	25	108	<b>L</b>
gi 53571 emb CAA25323.1	p53 [Mus musculus]	25	108	<b>L</b>
gi 18997097 gb AAL83290.1 AF475081.1	p53 [Delphinapterus le...	25	108	
gi 14039818 gb AAK53397.1 AF367373.1	p53 tumor suppressor (...)	25	108	
gi 28849929 ref NP_776626.1	p53 tumor suppressor phosphopr...	25	108	<b>L</b>
gi 3024331 sp P56423 P53_MACPA	Cellular tumor antigen p53 (...)	25	108	<b>S</b>
gi 2781308 pdb 1YCS A	Chain A, p53-53bp2 Complex	25	108	<b>L</b>
gi 642241 emb CAA25652.1	p53 [Homo sapiens]	25	108	<b>L</b>
gi 10720196 sp Q9W679 P53_TETMU	Cellular tumor antigen p53 ...	25	108	
gi 10720197 sp Q9WUR6 P53_CAVBO	Cellular tumor antigen p53 ...	25	108	
gi 506449 emb CAA42633.1	p53 transformation suppressor [Ho...	25	108	<b>L</b>
gi 129368 sp P10360 P53_CHICK	Cellular tumor antigen p53 (T...	25	108	
gi 1619833 gb AAB16961.1	p53 [Canis familiaris]	25	108	
gi 14719450 pdb 1HU8 A	Crystal Structure Of The Mo...	25	108	<b>S</b>
gi 506445 emb CAA42631.1	p53 transformation suppressor [Ho...	25	108	<b>L</b>
gi 5081783 gb AAD39535.1 AF151353.1	tumor suppressor p53 [M...	25	108	<b>L</b>
gi 10720190 sp Q36006 P53_MARMO	Cellular tumor antigen p53 ...	25	108	
gi 1223855 gb AA92052.1	p53 [Xiphophorus maculatus]	25	108	
gi 506443 emb CAA42630.1	p53 transformation suppressor [Ho...	25	108	<b>L</b>
gi 21730308 pdb 1GZH A	Chain A, Crystal Structure Of The Br...	25	108	<b>S</b>
gi 339814 gb AAB1211.1	p53 antigen	25	108	<b>L</b>
gi 2842741 sp Q95330 P53_RABIT	Cellular tumor antigen p53 (...)	25	108	
gi 1753089 gb AAB39322.1	cellular phosphoprotein p53	25	108	
gi 339816 gb AAB1212.1	p53 antigen	25	108	<b>L</b>
gi 10720193 sp Q92143 P53_XIPWA	Cellular tumor antigen p53 ...	25	108	
gi 506441 emb CAA42629.1	p53 transformation suppressor [Ho...	25	108	<b>L</b>
gi 6093639 sp Q29537 P53_CANFA	Cellular tumor antigen p53 (...)	25	108	
gi 10720192 sp Q93379 P53_ICRPU	Cellular tumor antigen p53 ...	25	108	
gi 1463021 gb AAC37335.1	p53 [Canis familiaris]	25	108	
gi 481535 pir S38824	cellular tumor antigen p53, minor spl...	25	108	<b>L</b>
gi 386994 gb AAA59987.1	phosphoprotein p53 [Homo sapiens]	25	108	<b>L</b>
gi 545102 gb AAC60746.1	p53 [Xenopus laevis]	25	108	
gi 10720191 sp Q57538 P53_XIPHE	Cellular tumor antigen p53 ...	25	108	

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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gi 20151154 pdb 1KZY A	Chain A, Crystal Structure Of The 53...	25	108	<b>S</b>
gi 3024332 sp P56424 P53_MACMU	Cellular tumor antigen p53 (...)	25	108	
gi 1310770 pdb 1TSR A	Chain A, p53 Core Domain In Complex W...	25	108	<b>S</b>
gi 1938365 gb AAB80959.1	mutant p53 [Rattus norvegicus]	25	108	<b>L</b>
gi 506439 emb CAA42628.1	p53 transformation suppressor [Ho...	25	108	<b>L</b>
gi 129367 sp P13481 P53_CERAE	Cellular tumor antigen p53 (T...	25	108	
gi 506451 emb CAA42634.1	p53 transformation suppressor [Ho...	25	108	<b>L</b>
gi 129371 sp P02340 P53_MOUSE	Cellular tumor antigen p53 (T...	25	108	<b>L</b>
gi 129373 sp P25035 P53_ONCMY	Cellular tumor antigen p53 (T...	25	108	
gi 468514 emb CAA54672.1	p53 [Xenopus laevis]	25	108	
gi 29468129 gb AA085406.1 AF365873.1	tumor suppressor p53 [...]	25	108	<b>L</b>
gi 4959054 gb AAD34214.1 AF071572.1	tumor suppressor protei...	25	108	
gi 26348179 dbj BAC37729.1	unnamed protein product [Mus mu...	25	108	<b>L</b>
gi 5755228 dbj BAA03927.1	p53 protein [Felis catus]	25	108	
gi 2465420 gb AAB72093.1	chimeric tumour suppressor [synth...	25	108	
gi 2833362 sp Q29480 P53_EQUAS	Cellular tumor antigen p53 (...)	25	108	
gi 2829679 sp P79892 P53_HORSE	Cellular tumor antigen p53 (...)	25	108	
gi 2842672 sp Q64662 P53_SPEBE	Cellular tumor antigen p53 (...)	25	108	
gi 506435 emb CAA42626.1	p53 transformation suppressor [Ho...	25	108	<b>L</b>
gi 23867780 dbj BAC21014.1	claudin42 [Xenopus laevis]	25	144	
gi 18150106 dbj BAB83668.1	insulin receptor [Paralichthys ...]	24	194	
gi 21623719 dbj BAC00941.1	HR-protein [Lycopersicon peruvl...]	24	260	
gi 17227039 gb AAL37982.1 AF442140.1	style-specific self-in...	24	260	
gi 21623726 dbj BAC00944.1	HR-A protein [Lycopersicon chm...	24	260	
gi 21623723 dbj BAC00943.1	HR-protein [Lycopersicon parvif...	24	260	

#### Alignments

Get selected sequences

>gi|31207283|ref|XP\_312608.1| ENSANGP00000014785 [Anopheles gambiae str. PESTR]  
gi|21295812|gb|EAA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PESTR]  
Length = 338

Score = 28.2 bits (59), Expect = 14  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 VCSCKPRD 9  
+CSCPKRD  
Sbjct: 310 ICSCPKRD 317

>gi|21355617|ref|NP\_651115.1| **L** CG10873-PA [Drosophila melanogaster]  
gi|7211767|gb|AAF40427.1|AF224713.1 **L** transcription factor p53 [Drosophila melano  
gi|7211769|gb|AAF40428.1|AF224714.1 **L** transcription factor p53 [Drosophila melano  
gi|7381624|gb|AAF61572.1|AF244918.1 **L** p53 tumor suppressor-like protein [Drosophi  
gi|8272608|gb|AAF74277.1|AF245918.1 **L** transcription factor [Drosophila melanogast  
gi|8453176|gb|AAF75270.1|AF263722.1 **L** transcription factor p53 [Drosophila melano  
gi|10726710|gb|AAF56087.2| **L** CG10873-PA [Drosophila melanogaster]

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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gi|17861528|gb|AAJ39241.1|**L** GH11591p [Drosophila melanogaster]  
gi|18032162|gb|AAJ56639.1|AF192555\_1 p53-like regulator of apoptosis and cell cys  
melanogaster]  
Length = 385

Score = 25.7 bits (53), Expect = 80  
Identities = 6/8 (75%), Positives = 8/8 (100%)

Query: 2 VCSCPKRD 9  
+C+CPKRD  
Sbjct: 260 ICTCPKRD 267

>gi|25009887|gb|AAW1112.1| AR28346p [Drosophila melanogaster]  
Length = 519

Score = 25.7 bits (53), Expect = 80  
Identities = 6/8 (75%), Positives = 8/8 (100%)

Query: 2 VCSCPKRD 9  
+C+CPKRD  
Sbjct: 394 ICTCPKRD 401

>gi|129372|sp|P10361|P53\_RAT Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|92070|pir|S02192 cellular tumor antigen p53 - rat  
gi|56829|emb|CAA31457.1|**L** nuclear protein p53 (AA 1 - 391) [Rattus norvegicus]  
Length = 391

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9  
RVC+CP RD  
Sbjct: 271 RVCACPGRD 279

>gi|7259331|dbj|BAA92786.1| p53 [Macaca fuscata]  
Length = 181

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9  
RVC+CP RD  
Sbjct: 148 RVCACPGRD 156

>gi|693787|gb|AAB31269.1| tumour suppressor [Canis familiaris]  
Length = 32

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9  
RVC+CP RD  
Sbjct: 4 RVCACPGRD 12

>gi|8400738|ref|NP\_000537.2|**L** tumor protein p53 [Homo sapiens]  
gi|625300|pir|DNH053 cellular tumor antigen p53 [validated] - human  
gi|35214|emb|CAA38095.1|**L** protein p53 [Homo sapiens]  
gi|506437|emb|CAA42627.1|**L** p53 transformation suppressor [Homo sapiens]  
gi|3041867|gb|AAC12971.1|**L** p53 [Homo sapiens]  
gi|4732147|gb|AAD28628.1|AF136271\_1 **L** tumor suppressor protein p53 [Homo sapiens]  
gi|11066970|gb|AAG28785.1|AF307851\_1 **L** p53 protein [Homo sapiens]  
Length = 393

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9  
RVC+CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|4959058|gb|AAD34216.1|AF071574\_1 tumor suppressor protein p53 [Oncomorphus]  
Length = 265

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9  
RVC+CP RD  
Sbjct: 252 RVCACPGRD 260

>gi|1709531|sp|P51664|P53\_SHEEP Cellular tumor antigen p53 (Tumor suppressor p5;  
gi|602357|emb|CAA57349.1| p53 [Ovis aries]  
Length = 382

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9  
RVC+CP RD  
Sbjct: 262 RVCACPGRD 270

>gi|129369|sp|P04637|P53\_HUMAN **L** Cellular tumor antigen p53 (Tumor suppressor p;  
p53) (Antigen NY-CO-13)  
gi|35210|emb|CAA26306.1|**L** p53 tumor antigen (aa 1-?) [Homo sapiens]  
gi|189476|gb|AA59988.1|**L** phosphoprotein p53  
gi|7595312|gb|AAF64408.1|AF192534\_1 tumor suppressor protein p53 [Expression vect  
Length = 393

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|1836145|gb|AAB46899.1| sequence-specific transcription factor (Equidae)  
Length = 263

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 224 RVCACPGRD 232

>gi|11321107|gb|AAG34052.1| p53 tumor suppressor [Rattus norvegicus]  
Length = 53

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 12 RVCACPGRD 20

>gi|16266760|dbj|BAB69969.1| p53 [Meriones unguiculatus]  
Length = 390

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 271 RVCACPGRD 279

>gi|21730310|pdb|1GZH|C [S] Chain C, Crystal Structure Of The Brct Domains Of Hum  
To The p53 Tumor Suppressor  
Length = 198

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 179 RVCACPGRD 187

>gi|6755881|ref|NP\_035770.1| [L] transformation related protein 53 [Mus musculus]  
gi|53576|emb|CAA25625.1| [L] p53 polypeptide (aa 1-390) [Mus musculus]

gi|871421|emb|CAA25420.1| [L] cellular tumour antigen p53 [Mus musculus]  
Length = 390

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|200201|gb|AAA39882.1| [L] p53  
Length = 390

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|1154648|emb|CAA62905.1| p53 [Equus caballus]  
Length = 196

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 140 RVCACPGRD 148

>gi|2811079|sp|O12946|P53\_PLAFL cellular tumor antigen p53 (Tumor suppressor p53;  
gi|1922902|emb|CAA70123.1| p53 [Platichthys flesus]  
Length = 366

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 248 RVCACPGRD 256

>gi|1171969|sp|P41685|P53\_FELICA cellular tumor antigen p53 (Tumor suppressor p53;  
gi|538225|dbj|BAA05653.1| p53 [Felis catus]  
Length = 386

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)



Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 266 RVCACPGRD 274

>gi|1000577|gb|AAB42022.1| p53 [Canis familiaris]  
Length = 276

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 237 RVCACPGRD 245

>gi|975651|emb|CAA62450.1| p53 [Callionymus lyra]  
Length = 45

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 37 RVCACPGRD 45

>gi|20900490|ref|XP\_128695.1| similar to transformation related protein 53 [M  
Length = 151

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 114 RVCACPGRD 122

>gi|8698976|gb|AAF78535.1|AF223795.1 tumor suppressor p53 [Oncorhynchus tshawytsch  
gi|8698978|gb|AAF78536.1|AF223796.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698980|gb|AAF78537.1|AF223797.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698982|gb|AAF78538.1|AF223798.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698984|gb|AAF78539.1|AF223799.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698986|gb|AAF78540.1|AF223800.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698988|gb|AAF78541.1|AF223801.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698990|gb|AAF78542.1|AF223802.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698992|gb|AAF78543.1|AF223803.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698994|gb|AAF78544.1|AF223804.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698996|gb|AAF78545.1|AF223805.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8698998|gb|AAF78546.1|AF223806.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699000|gb|AAF78547.1|AF223807.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699002|gb|AAF78548.1|AF223808.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699004|gb|AAF78549.1|AF223809.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699006|gb|AAF78550.1|AF223810.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699008|gb|AAF78551.1|AF223811.1 tumor suppressor p53 [Oncorhynchus tshawytscha

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

gi|8699010|gb|AAF78552.1|AF223812.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699012|gb|AAF78553.1|AF223813.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699014|gb|AAF78554.1|AF223814.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699016|gb|AAF78555.1|AF223815.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699018|gb|AAF78556.1|AF223816.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699020|gb|AAF78557.1|AF223817.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
gi|8699022|gb|AAF78558.1|AF223818.1 tumor suppressor p53 [Oncorhynchus tshawytscha  
Length = 146

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 42 RVCACPGRD 50

>gi|1729419|dbj|BAA08629.1| p53 gene product [Bos primigenius]  
Length = 374

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 254 RVCACPGRD 262

>gi|4731632|gb|AAD28535.1|AF135121.1 tumor suppressor protein p53 [Homo sapien  
Length = 393

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|10720195|gb|O9678|p53\_BARBU Cellular tumor antigen p53 (Tumor suppressor p  
gi|4959050|gb|AAD34212.1|AF071570.1 tumor suppressor protein p53 [Barbus barbus]  
Length = 369

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 237 RVCACPGRD 245

>gi|223827|ref|U001197A antigen p53, tumor  
Length = 390  
Score = 25.2 bits (52), Expect = 108

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003



Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|11342599|emb|CAC17147.1| **L** transformation related protein 53 [Mus musculus]  
Length = 307

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|18859503|ref|NP\_571402.1| **L** tumor protein p53; tumor suppressor homolog p53;  
antigen p53 [Danio rerio]  
gi|2829677|sp|E79734|P53\_BRARE Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|1778019|gb|AAB40617.1| **L** tumor suppressor p53 [Danio rerio]  
Length = 373

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 241 RVCACPGRD 249

>gi|10720186|sp|Q9TU92|P53\_PIG Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|6165623|gb|AAF04620.1|AF098067.1 tumor suppressor p53 [Sus scrofa]  
Length = 386

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 266 RVCACPGRD 274

>gi|2829194|gb|AAC26190.1| tumor suppressor ortholog [Xiphophorus maculatus]  
Length = 153

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 47 RVCACPGRD 55

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|4996230|dbj|BAJ78379.1| P53 [Canis familiaris]  
Length = 381

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 261 RVCACPGRD 269

>gi|13591878|ref|NP\_112251.1| **L** tumor protein p53; tumor protein p53 (Li-Fraumeni  
syndrome)  
gi|205952|gb|AAA41788.1| **L** tumor suppressor  
Length = 391

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 271 RVCACPGRD 279

>gi|129374|sp|P07193|P53\_XENLA Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|85718|pir|A29376 cellular tumor antigen p53 - African clawed frog  
gi|64962|emb|CAA28821.1| ORF (AA 1-363) [Xenopus laevis]  
gi|214640|gb|AAA4923.1| p53 protein homologue; putative  
Length = 363

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 248 RVCACPGRD 256

>gi|506453|emb|CAA42635.1| **L** p53 transformation suppressor [Homo sapiens]  
Length = 393

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|5353744|gb|AAD42225.1| p53 protein [Canis familiaris]  
Length = 246

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 156 RVCACPGRD 164

>gi|1389675|gb|AA18936.1| tumor-suppressor [Equus caballus]  
Length = 205

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 149 RVCACPGRD 157

>gi|2961247|gb|AAC05704.1| tumor suppressor p53 [Mus musculus]  
Length = 390

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|15375072|gb|AAK94783.1| transformation related protein 53 [Mus musculus]  
Length = 391

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|8698972|gb|AAF78533.1|AF223793.1 tumor suppressor p53 [Oncomorphus mykiss]  
gi|8698974|gb|AAF78534.1|AF223794.1 tumor suppressor p53 [Oncomorphus mykiss]  
Length = 146

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 42 RVCACPGRD 50

>gi|28975327|gb|AAO60156.1| tumor suppressor p53; p53as [Mus musculus]  
Length = 381

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|4959056|gb|AAD34215.1|AF071573.1 tumor suppressor protein p53 [Oncomorphus]  
Length = 265

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 252 RVCACPGRD 260

>gi|6841071|gb|AAF28891.1|AF124298.1 p53 protein [Sus scrofa]  
Length = 387

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 262 RVCACPGRD 270

>gi|53571|emb|CAA25323.1| p53 [Mus musculus]  
Length = 389

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 269 RVCACPGRD 277

>gi|18997097|gb|AA183290.1|AF475081.1 P53 [Delphinapterus leucas]  
Length = 387

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 267 RVCACPGRD 275

>gi|14039818|gb|AAK53397.1|AF367373.1 p53 tumor suppressor [Mus musculus]  
Length = 207

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 148 RVCACPGRD 156

>gi|28849929|ref|NP\_776626.1|L p53 tumor suppressor phosphoprotein [Bos taurus]  
gi|2499426|sp|Q29628.P53\_BOVIN Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|1083096|pir|S51648 cellular tumor antigen p53 - bovine  
gi|602333|emb|CAA57348.1|L p53 [Bos taurus]  
gi|1916676|gb|AA81214.1| 53 kDa phosphoprotein [Bos indicus]  
Length = 386

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 266 RVCACPGRD 274

>gi|3024331|sp|P56423.P53\_MACFA Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|2689467|gb|AA81535.1| P53 [Macaca fascicularis]  
Length = 393

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|2781308|pdb|1YCS|A S Chain A, p53-53bp2 Complex  
Length = 199

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 180 RVCACPGRD 188

>gi|642241|emb|CAA25652.1|L p53 [Homo sapiens]  
Length = 293

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPGRD 9  
RVC+CP RD  
Sbjct: 173 RVCACPGRD 181

Get selected sequences Select all Deselect all

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
Posted date: Jul 10, 2003 1:49 AM  
Number of letters in database: 474,244,320  
Number of sequences in database: 1,477,204

Lambda K H  
0.358 0.293 2.10  
Gapped  
Lambda K H  
0.294 0.110 0.610

Matrix: PAM30  
Gap Penalties: Existence: 9, Extension: 1  
Number of Hits to DB: 7,962,851  
Number of Sequences: 1477204  
Number of extensions: 43666  
Number of successful extensions: 1286  
Number of sequences better than 20000.0: 100  
Number of HSP's better than 20000.0 without gapping: 1235  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1286  
length of query: 9  
length of database: 474,244,320  
effective HSP length: 0  
effective length of query: 9  
effective length of database: 474,244,320  
effective search space: 4268198880  
effective search space used: 4268198880  
T: 11  
A: 40  
X1: 14 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 35 (19.8 bits)  
S2: 35 (18.0 bits)

EXHIBIT I

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:  
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,  
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),  
"Gapped BLAST and PSI-BLAST: a new generation of protein database search  
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057861714-02581-23117

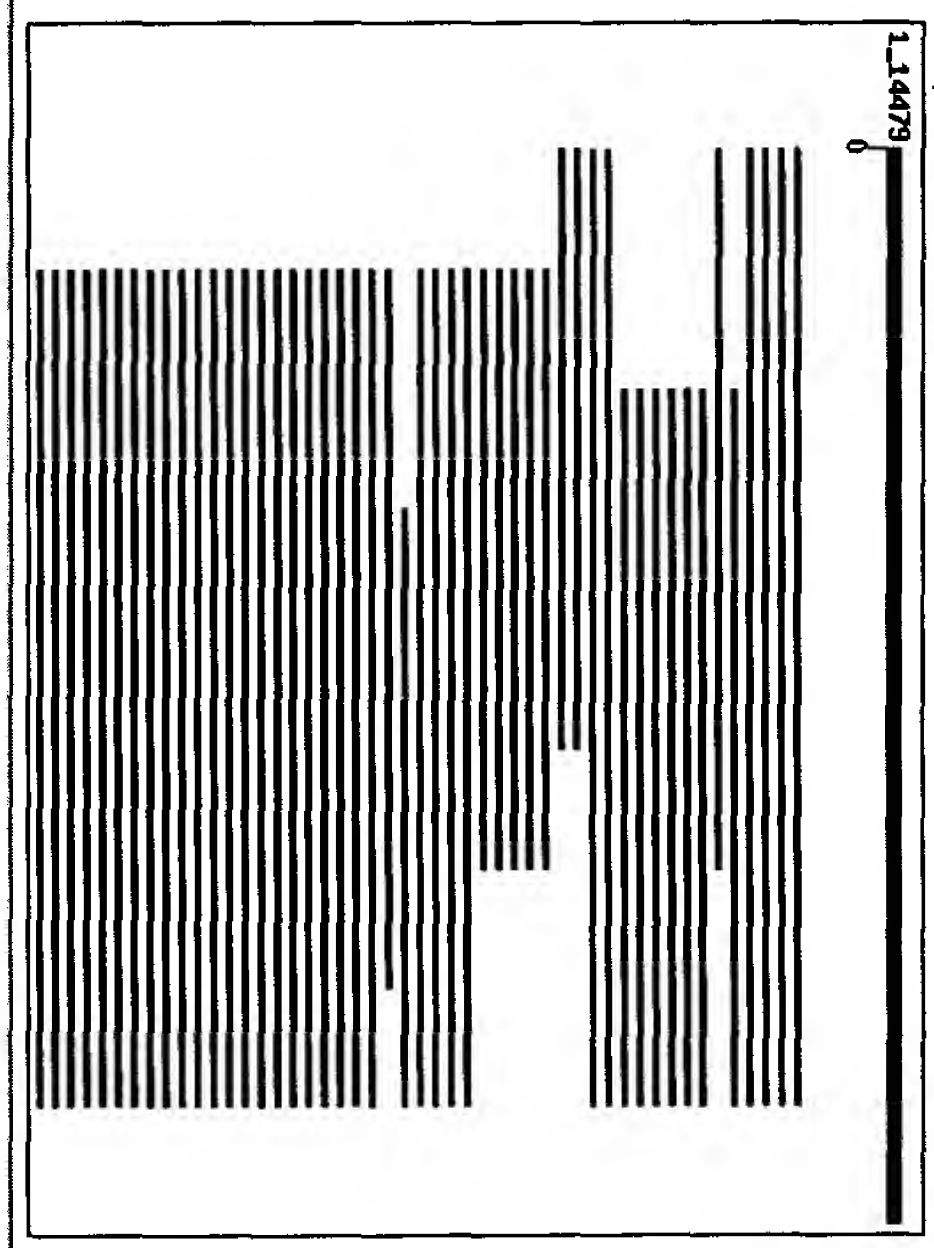
Query= SEQID26  
(9 letters)

Database: All non-redundant Genbank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQ](#)  
[Taxonomy reports](#)

Distribution of 111 Blast Hits on the Query Sequence

[Mouse-over to show define and scores. Click to show alignments](#)



Related Structures

Sequences producing significant alignments:

	Score	E
(bits) Value		
gi 31207283 ref XP_312608.1  ENSANGP00000014785 [Anopheles ...]	31	1.8
gi 21355617 ref NP_651115.1  CG10873-PA [Drosophila melanog...]	29	10
gi 25009887 gb AAW71112.1  AT28346p [Drosophila melanogaster]	29	10
gi 18150104 dbj BAB83667.1  insulin receptor [Paralichthys ...]	25	144
gi 23867780 dbj BAC21014.1  claudin4L2 [Xenopus laevis]	25	144
gi 21623719 dbj BAC00941.1  HT-protein [Lycopersicon peruv...	24	260
gi 17227039 gb AAI37982.1 AF442140.1 style-specific self-in...	24	260
gi 21623726 dbj BAC00944.1  HT-A protein [Lycopersicon chm...	24	260
gi 729929 sp P80424 LDT1_HIRME leech-derived tryptase inhib...	24	260
gi 21623723 dbj BAC00943.1  HT-protein [Lycopersicon parvif...	24	260
gi 21623729 dbj BAC00945.1  HT-A protein [Lycopersicon hirs...	24	260
gi 17227037 gb AAI37981.1 AF442139.1 style-specific self-in...	24	260
gi 8037578 gb AAI71401.1  serine proteinase inhibitor [Toxo...	24	349
gi 6957493 gb AAI32427.1 AF121778.1 tachyzoite serine prote...	24	349
gi 15418693 gb AAI91072.1  arrow [Drosophila melanogaster]	24	349
gi 24653390 ref NP_524737.2  arrow CG5912-PA [Drosophila me...	24	349
gi 1673504 emb CAA66181.1  G protein-coupled receptor kinas...	24	349
gi 7513209 pir G02453 NM8-4AG - human (fragment) >gi 12453...	24	349
gi 12621084 ref NP_075217.1  G protein-coupled receptor kin...	24	349
gi 17440180 ref XP_039548.2  similar to NM8-4AG [Homo sapiens]	24	349
gi 6760453 gb AAI28358.1 AF223365.1 LDL-related protein LRP...	24	349
gi 32451930 gb AAH54643.1  Unknown (protein for MGC:64214) ...	23	468
gi 31205795 ref XP_311849.1  ENSANGP00000018251 [Anopheles ...]	23	468

gi 24643447 ref NP_608372.1	CG572-PA (Drosophila melanoga...	23	468	<b>L</b>
gi 31235045 ref XP_319172.1	ENSANGP0000011831 [Anopheles ...	23	468	
gi 15236812 ref NP_194396.1	expressed protein [Arabidopsis...	23	468	
gi 2488235 sp Q91713 CHRD_XENLA	Chordin precursor (Organize...	22	843	
gi 129372 sp P10361 P53_PAF	Cellular tumor antigen p53 (Tum...	22	1131	<b>L</b>
gi 7259331 dbj BA92786.1	p53 [Macaca fuscata]	22	1131	
gi 189479 gb AA59989.1	p53 cellular tumor antigen	22	1131	<b>L</b>
gi 693787 gb AA31269.1	tumor suppressor (Canis familiaris)	22	1131	
gi 8400738 ref NP_000537.2	tumor protein p53 [Homo sapiens...	22	1131	<b>L</b>
gi 4959058 gb AAD34216.1 AF071574.1	tumor suppressor protei...	22	1131	
gi 1709531 sp P51664 P53_SHEEP	Cellular tumor antigen p53 (...)	22	1131	
gi 129369 sp P04637 P53_HUMAN	Cellular tumor antigen p53 (T...	22	1131	<b>L</b>
gi 1836145 gb AA846899.1	sequence-specific transcription f...	22	1131	
gi 11321107 gb AA34052.1	p53 tumor suppressor [Rattus nor...	22	1131	
gi 16266760 dbj BA869969.1	p53 [Meriones unguiculatus]	22	1131	
gi 21730310 pdb 1GZH C	Chain C, Crystal Structure of The Br...	22	1131	<b>S</b>
gi 6755881 ref NP_035770.1	transformation related protein ...	22	1131	<b>L</b>
gi 200201 gb AA39882.1	p53	22	1131	<b>L</b>
gi 1154648 emb CA62905.1	p53 [Equus caballus]	22	1131	
gi 2811079 sp O12946 P53_PLAIF	Cellular tumor antigen p53 (...)	22	1131	
gi 1171969 sp P41685 P53_FELCA	Cellular tumor antigen p53 (...)	22	1131	
gi 1000577 gb AA842022.1	p53 [Canis familiaris]	22	1131	
gi 976651 emb CA62450.1	p53 [Callionymus lyra]	22	1131	
gi 20900490 ref XP_128695.1	similar to transformation rela...	22	1131	<b>L</b>
gi 8698976 gb AA78535.1 AF223795.1	tumor suppressor p53 [On...	22	1131	
gi 1729419 dbj BA08629.1	p53 gene product [Bos primigenius]	22	1131	
gi 4731632 gb AAD8535.1 AF15121.1	tumor suppressor protei...	22	1131	<b>L</b>
gi 10720195 sp Q9W678 P53_BARBU	Cellular tumor antigen p53 ...	22	1131	
gi 223827 prf I001197A	antigen p53, tumor	22	1131	
gi 11342599 emb CAC17147.1	transformation related protein ...	22	1131	<b>L</b>
gi 18859503 ref NP_571402.1	tumor protein p53, tumor suppr...	22	1131	<b>L</b>
gi 10720186 sp Q9TUB2 P53_PIG	Cellular tumor antigen p53 (T...	22	1131	
gi 2829194 gb AAC26190.1	tumor suppressor ortholog [Xiphop...	22	1131	
gi 4996230 dbj BA78379.1	p53 [Canis familiaris]	22	1131	
gi 13591878 ref NP_112251.1	tumor protein p53, tumor prote...	22	1131	<b>L</b>
gi 129374 sp P07193 P53_XENLA	Cellular tumor antigen p53 (T...	22	1131	
gi 506453 emb CAA42635.1	p53 transformation suppressor [Ho...	22	1131	<b>L</b>
gi 5353744 gb ADA2225.1	p53 protein (Canis familiaris)	22	1131	
gi 23491729 dbj BA16799.1	p53 [Homo sapiens]	22	1131	<b>L</b>
gi 1389675 gb AA818936.1	tumor-suppressor [Equus caballus]	22	1131	
gi 2961247 gb AAC05704.1	tumor suppressor p53 [Mus musculus]	22	1131	<b>L</b>
gi 15375072 gb AA94783.1	transformation related protein 5...	22	1131	<b>L</b>
gi 8698972 gb AA78533.1 AF223793.1	tumor suppressor p53 [On...	22	1131	
gi 28975327 gb AA060156.1	tumor suppressor p53, p53as [Mus...	22	1131	<b>L</b>
gi 4959056 gb AAD34215.1 AF071573.1	tumor suppressor protei...	22	1131	
gi 6841071 gb AA78891.1 AF14298.1	p53 protein [Sus scrofa]	22	1131	
gi 53571 emb CAA25323.1	p53 [Mus musculus]	22	1131	<b>L</b>
gi 18997097 gb AA83290.1 AF475081.1	p53 [Delphinapterus le...	22	1131	
gi 14039818 gb AA53397.1 AF67373.1	p53 tumor suppressor (...)	22	1131	
gi 28849929 ref NP_776626.1	p53 tumor suppressor phosphopr...	22	1131	<b>L</b>
gi 3024331 sp P56423 P53_MACFA	Cellular tumor antigen p53 (...)	22	1131	<b>S</b>
gi 2781308 pdb 1YCS A	Chain A, p53-53bp2 Complex	22	1131	
gi 642241 emb CAA25652.1	p53 [Homo sapiens]	22	1131	<b>L</b>

gi 10720196 sp Q9W679 P53_TENMU	Cellular tumor antigen p53 ...	22	1131	
gi 10720197 sp Q9WUR6 P53_CAVPO	Cellular tumor antigen p53 ...	22	1131	
gi 506449 emb CAA42633.1	p53 transformation suppressor [Ho...	22	1131	<b>L</b>
gi 129368 sp P10360 P53_CHICK	Cellular tumor antigen p53 (T...	22	1131	
gi 1619833 gb AA816961.1	p53 [Canis familiaris]	22	1131	
gi 14719450 pdb 1H08 A	Chain A, Crystal Structure Of The Mo...	22	1131	<b>S</b>
gi 506445 emb CAA42631.1	p53 transformation suppressor [Ho...	22	1131	<b>L</b>
gi 5081783 gb AAD39535.1 AF151353.1	tumor suppressor p53 [M...	22	1131	<b>L</b>
gi 10720190 sp Q36006 P53_MARMO	Cellular tumor antigen p53 ...	22	1131	
gi 1223855 gb AA92052.1	p53 [Xiphophorus maculatus]	22	1131	
gi 506443 emb CAA42630.1	p53 transformation suppressor [Ho...	22	1131	<b>L</b>
gi 15215061 gb AAH12650.1	Cldn3 protein (Mus musculus)	22	1131	<b>L</b>
gi 21730308 pdb 1GZH A	Chain A, Crystal Structure Of The Br...	22	1131	<b>S</b>
gi 339814 gb AA61211.1	p53 antigen	22	1131	<b>L</b>
gi 2842741 sp Q95330 P53_RABIT	Cellular tumor antigen p53 (...)	22	1131	
gi 1753089 gb AA39322.1	cellular phosphoprotein p53	22	1131	
gi 339816 gb AA61212.1	p53 antigen	22	1131	<b>L</b>
gi 10720193 sp Q92143 P53_XIPMA	Cellular tumor antigen p53 ...	22	1131	
gi 506441 emb CAA42629.1	p53 transformation suppressor [Ho...	22	1131	<b>L</b>
gi 6093639 sp Q29537 P53_CANFA	Cellular tumor antigen p53 (...)	22	1131	
gi 10720192 sp Q93379 P53_ICTFU	Cellular tumor antigen p53 ...	22	1131	
gi 1463021 gb AAC37335.1	p53 [Canis familiaris]	22	1131	
gi 481535 pir S38824	cellular tumor antigen p53, minor spl...	22	1131	<b>L</b>
gi 386994 gb AA59987.1	phosphoprotein p53 [Homo sapiens]	22	1131	<b>L</b>

Alignments

Get selected sequences

Select all

Deselect all

>gi|31207283|ref|XP\_312608.1| ENSANGP0000014785 [Anopheles gambiae]  
 gi|21295812|gb|EAA07957.1| ENSANGP0000014785 [Anopheles gambiae str. PEST]  
 Length = 338

Score = 31.2 bits (66), Expect = 1.8  
 Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KVCSCPKRD 9  
 K+CSCPKRD  
 Subject: 309 KICSCPKRD 317

>gi|21355617|ref|NP\_651115.1| CG10873-PA [Drosophila melanogaster]  
 gi|7211767|gb|AAF40427.1|AF224713.1  
 gi|7211769|gb|AAF40428.1|AF224714.1  
 gi|7381624|gb|AA61572.1|AF244918.1  
 gi|8272608|gb|AAF74277.1|AF250918.1  
 gi|8453176|gb|AAF75270.1|AF263722.1  
 gi|10726710|gb|AAF56087.2|  
 gi|17861528|gb|AAL39241.1|  
 CG10873-PA [Drosophila melanogaster]  
 transcription factor p53 [Drosophila melano]  
 transcription factor p53 [Drosophila melano]  
 p53 tumor suppressor-like protein [Drosophi]  
 transcription factor [Drosophila melanogast]  
 transcription factor p53 [Drosophila melano]  
 GH11591p [Drosophila melanogaster]

[gi|18032162|gb|AA156639.1|AF192555.1](#) p53-like regulator of apoptosis and cell cyc  
melanogaster]  
Length = 385

Score = 28.6 bits (60), Expect = 10  
Identities = 7/9 (77%), Positives = 9/9 (100%)

Query: 1 KVCSCPKRD 9  
K+C+CPKRD  
Sbjct: 259 KICTCPKRD 267

[gi|25009887|gb|AAW71112.1](#) AT28346p [Drosophila melanogaster]  
Length = 519

Score = 28.6 bits (60), Expect = 10  
Identities = 7/9 (77%), Positives = 9/9 (100%)

Query: 1 KVCSCPKRD 9  
K+C+CPKRD  
Sbjct: 393 KICTCPKRD 401

[gi|18150104|dbj|BA83667.1](#) insulin receptor [Paralichthys olivaceus]  
Length = 1369

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 KVCSCPKRD 9  
KVC+CPK D  
Sbjct: 705 KVCACPKRD 713

[gi|23867780|dbj|BAC21014.1](#) claudin4L2 [Xenopus laevis]  
Length = 213

Score = 24.8 bits (51), Expect = 144  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9  
CSCPKR+  
Sbjct: 183 CSCPKRE 189

[gi|21623719|dbj|BAC00941.1](#) HT-protein [Lycopersicon peruvianum]  
Length = 96

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9  
CSCPK+D  
Sbjct: 61 CSCPKRD 67

[gi|17227039|gb|AA137982.1|AF442140.1](#) style-specific self-incompatibility putat;  
HT-A2 [Solanum chacoense]  
Length = 77

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9  
CSCPK+D  
Sbjct: 44 CSCPKKD 50

[gi|21623726|dbj|BAC00944.1](#) HT-A protein [Lycopersicon chmielewskii]  
Length = 89

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9  
CSCPK+D  
Sbjct: 55 CSCPKKD 61

[gi|729929|sp|P80424|LDPI\\_HIRME](#) leech-derived trypase inhibitor (LDPI)  
[gi|7511702|pir|S50015](#) leech-derived trypase inhibitor - medicinal leech  
[gi|3212564|pdb|1DDT|L](#) Chain L, Complex Of Leech-Derived Trypase Inhibitor With  
Porcine Trypsin  
[gi|3318723|pdb|1ANI|I](#) Chain I, leech-Derived Trypase InhibitorTRYPSIN COMPLEX  
[gi|998917|gb|AA833769.1](#) master cell trypase inhibitor, LDPI [Hirudo  
medicinalis=medical leeches, Peptide, 46 aa]  
Length = 46

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 1 KVCSCPK 7  
KVC+CPK  
Sbjct: 2 KVCACPK 8

[gi|21623723|dbj|BAC00943.1](#) HT-protein [Lycopersicon parviflorum]  
Length = 90

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9  
CSCPK+D  
Sbjct: 55 CSCPKKD 61

[gi|21623729|dbj|BAC00945.1](#) HT-A protein [Lycopersicon hirsutum]



Length = 84

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPARD 9  
CSCP+D  
Sbjct: 50 CSCPARD 56

>gi|17227037|gb|AA137981.1|AF442139.1 style-specific self-incompatibility putati  
HT-A1 (Solanum chacoense)  
Length = 99

Score = 24.0 bits (49), Expect = 260  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPARD 9  
CSCP+D  
Sbjct: 66 CSCPARD 72

>gi|8037578|gb|AA71401.1| serine proteinase inhibitor (Toxoplasma gondii)  
Length = 62

Score = 23.5 bits (48), Expect = 349  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 1 KVCSCP 6  
KVCSCP  
Sbjct: 21 KVCSCP 26

>gi|6957493|gb|AA732427.1|AF121778.1 tachyzoite serine proteinase inhibitor (To  
Length = 294

Score = 23.5 bits (48), Expect = 349  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 1 KVCSCP 6  
KVCSCP  
Sbjct: 28 KVCSCP 33

>gi|15418693|gb|AA791072.1| arrow [Drosophila melanogaster]  
Length = 1678

Score = 23.5 bits (48), Expect = 349  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCSCP 7  
VCSCP  
Sbjct: 1297 VCSCP 1302

>gi|24653390|ref|NP\_524737.2| arrow CG5912-PA [Drosophila melanogaster]  
gi|21627234|gb|AA758373.2| CG5912-PA [Drosophila melanogaster]  
Length = 1678

Score = 23.5 bits (48), Expect = 349  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCSCP 7  
VCSCP  
Sbjct: 1297 VCSCP 1302

>gi|1673504|emb|CA66181.1| G protein-coupled receptor kinase GRK4B [Rattus no  
Length = 544

Score = 23.5 bits (48), Expect = 349  
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

Query: 1 KVCSC---PKRD 9  
K+CSC PKR+  
Sbjct: 508 KICSCILRPKRN 519

>gi|7513209|pir|G02453| NN8-4AG - human (fragment)  
gi|1245372|gb|AA838131.1| NN8-4AG  
Length = 412

Score = 23.5 bits (48), Expect = 349  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCSCP 7  
VCSCP  
Sbjct: 369 VCSCP 374

>gi|12621084|ref|NP\_075217.1| G protein-coupled receptor kinase 2, groucho gei  
norvegicus)  
gi|1673503|emb|CA66180.1| G protein-coupled receptor kinase GRK4A [Rattus norv

Length = 575

Score = 23.5 bits (48), Expect = 349  
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

Query: 1 KVCSC---PKRD 9  
K+CSC PKR+  
Sbjct: 539 KICSCILRPKRN 550

>gi|17440180|ref|XP\_039548.2| similar to NN8-4AG [Homo sapiens]  
Length = 418

Score = 23.5 bits (48), Expect = 349



Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCSCP 7

Sbjct: 375 VCSCP 380

☐ >gi|6760453|gb|AAF28358.1|AF223365.1 ☒ LDL-related protein LRP6 [Drosophila mel; Length = 1678

Score = 23.5 bits (48), Expect = 349  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCSCP 7

Sbjct: 1297 VCSCP 1302

☐ >gi|32451930|gb|AAH54643.1| unknown (protein for MCC:64214) [Danio rerio]  
Length = 579

Score = 23.1 bits (47), Expect = 468  
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 2/10 (20%)

Query: 2 VCSCP--KRD 9

Sbjct: 46 VCSCP LCKRE 55

☐ >gi|31205795|ref|XP\_311849.1| ENSANGP0000018251 [Anopheles gambiae]  
gi|30177281|gb|EAA07856.2| ENSANGP0000018251 [Anopheles gambiae str. PEST]  
Length = 465

Score = 23.1 bits (47), Expect = 468  
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 1/8 (12%)

Query: 2 VCSCP KRD 9

Sbjct: 324 VCSCP-RD 330

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 164 VCSCP 168

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

VCSCP

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Sbjct: 105 VCSCP 109

Score = 19.3 bits (38), Expect = 6602  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 2 VCSCP 7

Sbjct: 265 VCECPK 270

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 431 VCTCP 435

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 372 VCTCP 376

☐ >gi|24643447|ref|NP\_608372.1| ☒ CG9572-PA [Drosophila melanogaster]  
gi|7289281|gb|AAF45369.1| ☒ CG9572-PA [Drosophila melanogaster]  
Length = 441

Score = 23.1 bits (47), Expect = 468  
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 1/8 (12%)

Query: 2 VCSCP KRD 9

Sbjct: 307 VCSCP-RD 313

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 146 VCSCP 150

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 87 VCSCP 91

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 19.3 bits (38), Expect = 6602  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 2 VCSCP 7  
VC CPK  
Sbjct: 248 VCECPK 253

>gi|31235045|ref|XP\_319172.1| ENSANGP00000011831 [Anopheles gambiae]  
gi|21301731|gb|EAA13876.1| ENSANGP00000011831 [Anopheles gambiae str. PEST]  
Length = 2212

Score = 23.1 bits (47), Expect = 468  
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 1/8 (12%)

Query: 2 VCSCP 9  
VCSCP RD  
Sbjct: 100 VCSCP-RD 106

Score = 21.0 bits (42), Expect = 2037  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCSCP 8  
VCSCP R  
Sbjct: 188 VCSCP 194

Score = 18.5 bits (36), Expect = 11887  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCSCP 6  
+CSCP  
Sbjct: 514 ICSCP 518

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCSCP 6  
VC+CP  
Sbjct: 903 VCNCP 907

>gi|15236812|ref|NP\_194396.1| expressed protein [Arabidopsis thaliana]  
gi|7487040|pir|T08932| hypothetical protein T15N24.110 - Arabidopsis thaliana  
gi|4938504|emb|CA43862.1| putative protein [Arabidopsis thaliana]  
gi|7269518|emb|CA879521.1| putative protein [Arabidopsis thaliana]  
Length = 806

Score = 23.1 bits (47), Expect = 468

Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 4 SCP 9  
SCP RD  
Sbjct: 184 SCP 189

>gi|2498235|sp|Q91713|CHRD\_XENLA Chordin precursor (Organizer-specific secreted  
gi|1072455|pir|A55195| chordin precursor - African clawed frog  
gi|603945|gb|AAC42222.1| chordin  
Length = 941

Score = 22.3 bits (45), Expect = 843  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCSCP 8  
VCSC KR  
Sbjct: 716 VCSCQR 722

>gi|129372|sp|P10361|P53\_RAT Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|92070|pir|S02192| cellular tumor antigen p53 - rat  
gi|56829|emb|CAA31457.1| nuclear protein p53 (AA 1 - 391) [Rattus norvegicus]  
Length = 391

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCP 9  
VC+CP RD  
Sbjct: 272 VCACPRD 279

>gi|7259331|dbj|BAA92786.1| p53 [Macaca fuscata]  
Length = 181

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCP 9  
VC+CP RD  
Sbjct: 149 VCACPRD 156

>gi|189479|gb|AA45989.1| p53 cellular tumor antigen  
Length = 393

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCP 9  
VC+CP RD  
Sbjct: 274 VCACPRD 281

gi|693787|gb|AAB31269.1| tumour suppressor [Canis familiaris]  
Length = 32  
Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)  
Query: 2 VCSCPRKD 9  
VC+CP RD  
Sbjct: 5 VCACPRGD 12

gi|8400738|ref|NP\_000537.2| tumor protein p53 [Homo sapiens]  
gi|625300|pir|DNH053 cellular tumor antigen p53 [validated] - human  
gi|35214|emb|CAA38095.1| protein p53 [Homo sapiens]  
gi|506437|emb|CAA42627.1| p53 transformation suppressor [Homo sapiens]  
gi|3041867|gb|AAC12971.1| p53 [Homo sapiens]  
gi|4732147|gb|AAD28628.1|AF136271.1 tumor suppressor protein p53 [Homo sapiens]  
gi|11066970|gb|AAG28785.1|AF307851.1 p53 protein [Homo sapiens]  
Length = 393

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)  
Query: 2 VCSCPRKD 9  
VC+CP RD  
Sbjct: 274 VCACPRGD 281

gi|4959058|gb|AAD34216.1|AF071574.1 tumor suppressor protein p53 [Oncomorphus]  
Length = 265  
Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRKD 9  
VC+CP RD  
Sbjct: 253 VCACPRGD 260

gi|1709531|sp|P51664|P53\_SHEEP Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|602357|emb|CAA57349.1| p53 [Ovis aries]  
Length = 382  
Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRKD 9  
VC+CP RD  
Sbjct: 263 VCACPRGD 270

gi|129369|sp|P04637|P53\_HUMAN Cellular tumor antigen p53 (Tumor suppressor p53) (Antigen NY-CO-13)  
gi|35210|emb|CAA26306.1| p53 tumor antigen (aa 1-?) [Homo sapiens]  
gi|189476|gb|AA59988.1| phosphoprotein p53  
gi|7595312|gb|AAF64408.1|AF192534.1 tumor suppressor protein p53 [Expression vect]  
Length = 393

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)  
Query: 2 VCSCPRKD 9  
VC+CP RD  
Sbjct: 274 VCACPRGD 281

gi|1836145|gb|AAB46899.1| sequence-specific transcription factor [Equidae]  
Length = 263  
Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)  
Query: 2 VCSCPRKD 9  
VC+CP RD  
Sbjct: 225 VCACPRGD 232

gi|11321107|gb|AAG34052.1| p53 tumor suppressor [Rattus norvegicus]  
Length = 53

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)  
Query: 2 VCSCPRKD 9  
VC+CP RD  
Sbjct: 13 VCACPRGD 20

gi|16266760|dbj|BAB69969.1| p53 [Meriones unguiculatus]  
Length = 390

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)  
Query: 2 VCSCPRKD 9  
VC+CP RD  
Sbjct: 272 VCACPRGD 279

gi|21730310|pdb|1GZH|C Chain C, Crystal Structure Of The Bcr1 Domains Of Hum  
To The P53 Tumor Suppressor  
Length = 198  
Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 180 VCACPGRD 187

>gi|6755881|ref|NP\_035770.1| L transformation related protein 53 [Mus musculus]  
gi|53576|emb|CAA25625.1| L p53 polypeptide (aa 1-390) [Mus musculus]  
gi|871421|emb|CAA25420.1| L cellular tumour antigen p53 [Mus musculus]  
Length = 390

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 271 VCACPGRD 278

>gi|200201|gb|AAA39882.1| L p53  
Length = 390

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 271 VCACPGRD 278

>gi|1154648|emb|CAA62905.1| p53 [Equus caballus]  
Length = 196

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 141 VCACPGRD 148

>gi|2811079|sp|O12946|p53\_PLAFL Cellular tumor antigen p53 (Tumor suppressor p53;  
gi|1922902|emb|CAA70123.1| p53 [Platichthys flesus]  
Length = 366

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 249 VCACPGRD 256

>gi|1171969|sp|P41685|p53\_FELCA Cellular tumor antigen p53 (Tumor suppressor p53;  
gi|538225|dbj|BA05653.1| p53 [Felis catus]  
Length = 386

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 267 VCACPGRD 274

>gi|100577|gb|AAB42022.1| p53 [Canis familiaris]  
Length = 276

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 238 VCACPGRD 245

>gi|975651|emb|CAA62450.1| p53 [Callionymus lyra]  
Length = 45

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 38 VCACPGRD 45

>gi|20900490|ref|XP\_128695.1| L similar to transformation related protein 53 [M  
Length = 151

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPKRD 9  
VC+CP RD  
Sbjct: 115 VCACPGRD 122

>gi|8698976|gb|AAF78535.1|AF223795.1 tumor suppressor p53 [Oncomyrmecops tshawytsch  
gi|8698978|gb|AAF78536.1|AF223796.1 tumor suppressor p53 [Oncomyrmecops tshawytsch  
gi|8698980|gb|AAF78537.1|AF223797.1 tumor suppressor p53 [Oncomyrmecops tshawytsch  
gi|8698982|gb|AAF78538.1|AF223798.1 tumor suppressor p53 [Oncomyrmecops tshawytsch  
gi|8698984|gb|AAF78539.1|AF223799.1 tumor suppressor p53 [Oncomyrmecops tshawytsch  
gi|8698986|gb|AAF78540.1|AF223800.1 tumor suppressor p53 [Oncomyrmecops tshawytsch  
gi|8698988|gb|AAF78541.1|AF223801.1 tumor suppressor p53 [Oncomyrmecops tshawytsch  
gi|8698990|gb|AAF78542.1|AF223802.1 tumor suppressor p53 [Oncomyrmecops tshawytsch  
gi|8698992|gb|AAF78543.1|AF223803.1 tumor suppressor p53 [Oncomyrmecops tshawytsch

gi 8698994 gb AAE78544.1 AF223804_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8698996 gb AAE78545.1 AF223805_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8698998 gb AAE78546.1 AF223806_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699000 gb AAE78547.1 AF223807_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699002 gb AAE78548.1 AF223808_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699004 gb AAE78549.1 AF223809_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699006 gb AAE78550.1 AF223810_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699008 gb AAE78551.1 AF223811_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699010 gb AAE78552.1 AF223812_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699012 gb AAE78553.1 AF223813_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699014 gb AAE78554.1 AF223814_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699016 gb AAE78555.1 AF223815_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699018 gb AAE78556.1 AF223816_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699020 gb AAE78557.1 AF223817_1	tumor suppressor p53 [Oncothynchus tshawytscha
gi 8699022 gb AAE78558.1 AF223818_1	tumor suppressor p53 [Oncothynchus tshawytscha

Length = 146

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPGRD 9  
VC+CP RD  
Sbjct: 43 VCACPGRD 50

>gi|1729419|dbj|BAA08629.1| p53 gene product [Bos primigenius]  
Length = 374

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPGRD 9  
VC+CP RD  
Sbjct: 255 VCACPGRD 262

>gi|4731632|gb|AAD28535.1|AF15121\_1 tumor suppressor protein p53 [Homo sapiens]  
Length = 393

Score = 21.8 bits (44), Expect = 1131  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPGRD 9  
VC+CP RD  
Sbjct: 274 VCACPGRD 281

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
Posted date: Jul 10, 2003 1:49 AM  
Number of letters in database: 474,244,320

Number of sequences in database: 1,477,204

Lambda K H  
0.361 0.293 2.09  
Gapped K H  
Lambda 0.294 0.110 0.610

Matrix: PAM30  
Gap Penalties: Existence: 9, Extension: 1  
Number of Hits to DB: 7,988,641  
Number of Sequences: 1477204  
Number of extensions: 38359  
Number of successful extensions: 1191  
Number of sequences better than 20000.0: 100  
Number of HSP's better than 20000.0 without gapping: 1132  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1191  
Length of query: 9  
Length of database: 474,244,320  
effective HSP length: 0  
effective length of query: 9  
effective length of database: 474,244,320  
effective search space: 4268198880  
effective search space used: 4268198880  
T: 11  
A: 40  
X1: 14 (7.3 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 35 (20.0 bits)  
S2: 35 (18.0 bits)



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057869455-01002-4505

Query: SEQID27  
(9 letters)

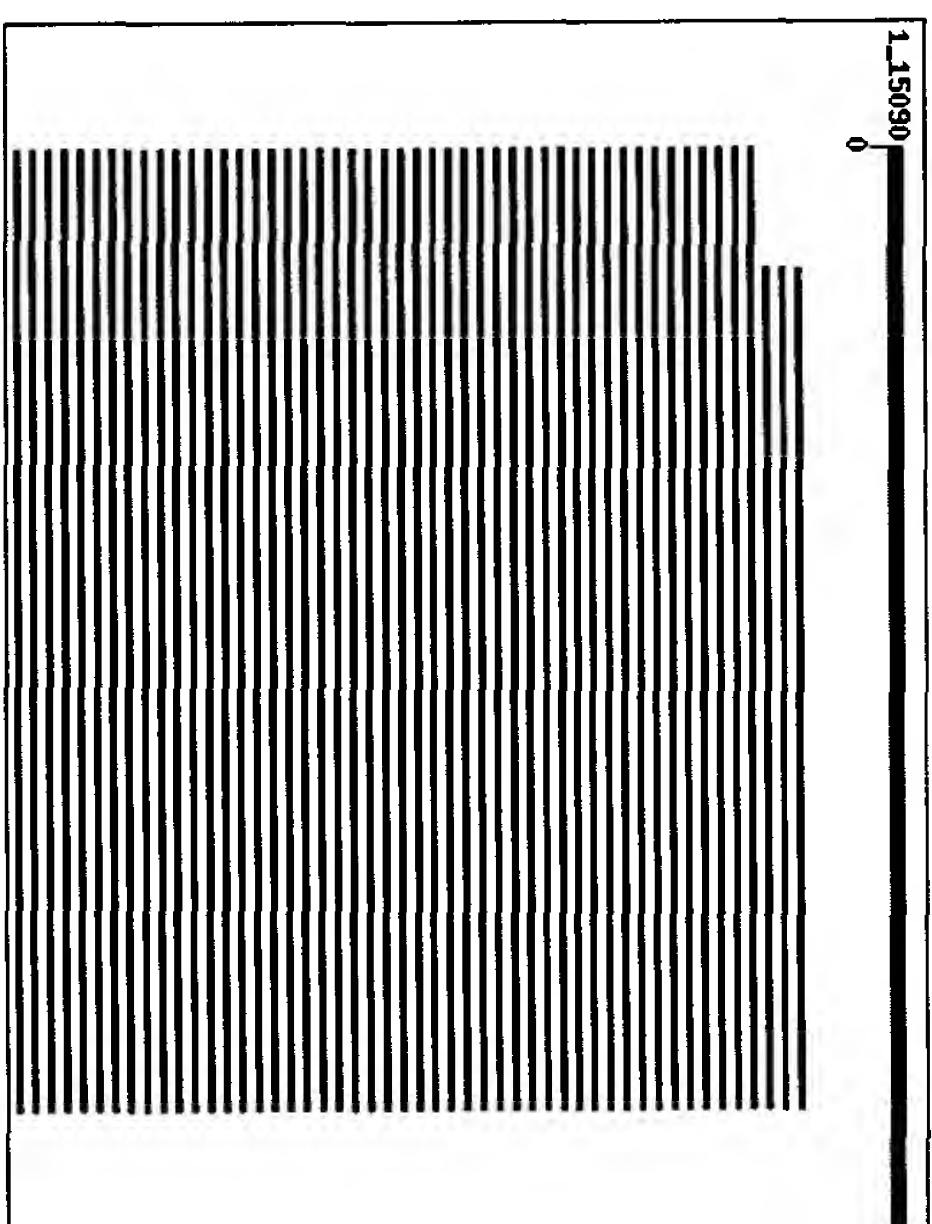
Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

Distribution of 112 Blast Hits on the Query Sequence

[Mouse-over to show define and scores. Click to show alignments](#)



Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi 21355617 ref NP_651115.1	31	1.8
gi 25009887 gb AA071112.1	31	1.8
gi 31207283 ref XP_312608.1	28	14
gi 3695096 gb AAC62642.1	25	108
gi 13751181 emb CAC37102.1	25	108
gi 13751173 emb CAC37098.1	25	108
gi 20428532 gb AA081886.1	25	108
gi 1813455 gb AA041833.1	25	108
gi 19909983 dbj BAB87245.1	25	108
gi 7248451 gb AA03492.1	25	108
gi 20892181 ref XP_147232.1	25	108
gi 3695094 gb AAC62641.1	25	108
gi 12060406 dbj BAB20591.1	25	108
gi 4803651 emb CAA72225.1	25	108
gi 13751179 emb CAC37101.1	25	108
gi 15072750 emb CAC48053.1	25	108
gi 29470179 gb AA074632.1	25	108
gi 2581764 gb AA082420.1	25	108
gi 8217484 emb CAB92742.1	25	108
gi 2370178 emb CAA72221.1	25	108
gi 21264484 sp P79820 P53	25	108
gi 1184759 gb AA087577.1	25	108
gi 1184757 gb AA087576.1	25	108
gi 7248450 gb AA03491.1	25	108
CG10873-PA [Drosophila melanogaster]		
AT28346p [Drosophila melanogaster]		
ENSANGP0000014785 [Anopheles ...]		
DN p63 gamma [Mus musculus]		
DN p63 gamma protein [Rattus no...		
TA1 KER alpha protein [Rattus n...		
DN p73 gamma [Homo sapiens]		
p53		
deltan p73 beta [Homo sapiens] ...		
p51 isoform delNbeta [Homo sapiens]		
transformation related protein...		
TA*p63 alpha [Mus musculus]		
delta N p73L [Homo sapiens]		
p73 splice variant [Cercopithec...		
TA2 KER gamma protein [Rattus n...		
p63 delta [Homo sapiens]		
p73 [Danio rerio]		
p53 [Cricetulus griseus]		
delta1092A11.2 (tumor protein p73) ...		
second splice variant [Homo sapi...		
ORYL A Cellular tumor antigen p53 ...		
p53 tumor suppressor homolog		
p53 tumor suppressor homolog		
p51 isoform delNalpha [Homo sapiens]		



gi 72484447 gb AAAF3448.1	p51 isoform TAP63beta (Homo sapiens)	25	108	
gi 32737451 gb AAC24830.1	p53 homolog (Homo sapiens)	25	108	<b>L</b>
gi 4735791 gb AAB41344.1	tumor suppressor p53 [Mesocricetus ...]	25	108	
gi 27527178 emb CAD10682.1	p53 protein [Monodelphis domestica]	25	108	
gi 12024746 gb AAC45609.1	TA p63 gamma (Homo sapiens)	25	108	
gi 3695098 gb AAC62643.1	DN p63 beta [Mus musculus]	25	108	<b>L</b>
gi 4689086 gb AAD27752.1	AF043641.1 p73 (Barbus barbatus)	25	108	
gi 6755883 ref NP_035771.1	transformation related protein ...	25	108	<b>L</b>
gi 1244762 gb AAAF8563.1	p53 tumor suppressor homolog	25	108	
gi 13751187 emb CAC37105.1	DN KET beta protein [Rattus nor...	25	108	<b>L</b>
gi 23308709 ref NP_694518.1	deltaNP63 isoform alpha 1; tum...	25	108	<b>L</b>
gi 26339452 dbj BAC33397.1	unnamed protein product [Mus mu...	25	108	<b>L</b>
gi 23308711 ref NP_694519.1	deltaNP63 isoform gamma; tumor...	25	108	<b>L</b>
gi 3695082 gb AAC62635.1	TA p63 alpha (Homo sapiens)	25	108	<b>L</b>
gi 1698502 gb AAC60146.1	p53 [Oryzias latipes] >gi 1208249...	25	108	
gi 20850793 ref XP_131858.1	transformation related protein...	25	108	<b>L</b>
gi 13195250 gb AAK15622.1	AF314148.1 p63 DNA binding protei...	25	108	
gi 3510328 dbj BAA32592.1	p51A (Homo sapiens) >gi 3695078 ...	25	108	<b>L</b>
gi 13751185 emb CAC37104.1	TA1 KET beta protein [Rattus no...	25	108	<b>L</b>
gi 451931 gb AAAF37086.1	tumor suppressor protein [Mesocric...	25	108	
gi 1813453 gb AAB41832.1	p53	25	108	<b>L</b>
gi 3695080 gb AAC62634.1	DN p63 gamma (Homo sapiens) >gi 7...	25	108	<b>L</b>
gi 1813451 gb AAB41831.1	p53	25	108	
gi 3970717 emb CAA76562.1	KET protein (Homo sapiens)	25	108	<b>L</b>
gi 23308685 ref NP_689454.1	deltaNP63 isoform alpha 2; tum...	25	108	<b>L</b>
gi 3445484 dbj BAA32433.1	p73H (Homo sapiens)	25	108	<b>L</b>
gi 7689271 gb AAF67733.1	AF233323.1 p53 tumor suppressor-li...	25	108	
gi 17985367 gb AAAF50211.1	tumor protein [Canis familiaris]	25	108	
gi 31543818 ref NP_003713.3	tumor protein p73-like; tumor ...	25	108	<b>L</b>
gi 19909981 dbj BAB87244.1	deltaNP73 alpha (Homo sapiens)...	25	108	<b>L</b>
gi 4101546 gb AAD01196.1	tumor suppressor protein p53 [Ory...	25	108	
gi 1813457 gb AAB41834.1	p53	25	108	
gi 1244764 gb AAAF8564.1	p53 tumor suppressor homolog	25	108	
gi 7440008 pir JC6176	tumor suppressor protein p53 - Chine...	25	108	
gi 12856636 dbj BAB30732.1	unnamed protein product [Mus mu...	25	108	<b>L</b>
gi 19850152 gb AAAF9584.1	AF285104.1 p53-like transcription...	25	108	
gi 7320915 emb CAB81954.1	p73 delta-N protein [Mus musculus]	25	108	<b>L</b>
gi 1293701 sp Q00366 P53_MESAV	Cellular tumor antigen p53 (T...	25	108	
gi 7689273 gb AAF67734.1	AF253324.1 p73-like protein [Mya a...	25	108	
gi 3695088 gb AAC62638.1	DN p63 beta (Homo sapiens) >gi 12...	25	108	<b>L</b>
gi 2370177 emb CAA72219.1	first splice variant (Homo sapiens)	25	108	<b>L</b>
gi 3510330 dbj BAA32593.1	p51B (Homo sapiens) >gi 7248446 ...	25	108	<b>L</b>
gi 1890327 emb CAA70109.1	p53 tumor suppressor [Cricetulu...	25	108	
gi 7248452 gb AAF43493.1	p51 isoform delNdelta (Homo sapiens)	25	108	
gi 12060487 dbj BAB20631.1	DN p63 alpha [Gallus gallus]	25	108	
gi 3695092 gb AAC62640.1	TA*p63 beta [Mus musculus]	25	108	<b>L</b>
gi 10720194 sp Q9TAA1 P53_TUGB	Cellular tumor antigen p53 ...	25	108	
gi 7248448 gb AAF43489.1	p51 isoform TAP63delta (Homo sapi...	25	108	<b>L</b>
gi 3695090 gb AAC62639.1	TA*p63 gamma [Mus musculus]	25	108	
gi 2499428 sp O09185 P53_CRIGR	Cellular tumor antigen p53 (...)	25	108	
gi 12643523 sp Q9XSK8 P73_CERAE	tumor protein p73 (p53-like...	25	108	

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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gi 4885645 ref NP_005418.1	tumor protein p73; p53-related ...	25	108	<b>L</b>
gi 12024745 gb AAG45608.1	TA p63 beta (Homo sapiens)	25	108	
gi 9507209 ref NP_062094.1	transformation related protein ...	25	108	<b>L</b>
gi 3695086 gb AAC62637.1	TA p63 beta (Homo sapiens)	25	108	<b>L</b>
gi 4887145 gb AAD32213.1	p73 [Mus musculus]	25	108	<b>L</b>
gi 13751183 emb CAC37103.1	TA2 KET beta protein [Rattus no...	25	108	<b>L</b>
gi 3644040 gb AAC43038.1	CUSP (Homo sapiens) >gi 3695084 g...	25	108	<b>L</b>
gi 13751177 emb CAC37100.1	TA1 KET gamma protein [Rattus n...	25	108	<b>L</b>
gi 22993563 ref ZP_00038140.1	hypothetical protein [Xylella...	25	144	
gi 15824372 gb AAAF09310.1	AF302499.1 death receptor 6 [Salv...	25	144	
gi 1352528 sp Q01705 NTC1_MOUSE	Neurogenic locus notch homo...	25	144	<b>L</b>
gi 1709335 sp P21783 NOTC_XENTLA	Neurogenic locus notch prot...	24	194	
gi 18859115 ref NP_571516.1	notch homolog 1a; neurogenic 1...	24	194	<b>L</b>
gi 27675874 ref XP_228125.1	similar to 40kDa ribosomal pro...	24	194	<b>L</b>
gi 1042521 pir A35844	Xotch protein - African clawed frog	24	194	
gi 22966887 ref ZP_00014482.1	hypothetical protein [Rhodos...	23	468	
gi 8928081 sp Q92A11 DHAL_RHORU	Aldehyde dehydrogenase >gi ...	23	468	
gi 21238945 dbj BAB96577.1	aldehyde dehydrogenase [Cytopha...	23	468	
gi 23113187 ref ZP_00098587.1	hypothetical protein [Desulf...	23	468	
gi 1293732 sp P10361 P53_RAT	Cellular tumor antigen p53 (Tum...	23	628	<b>L</b>
gi 7559331 dbj BAA92786.1	p53 [Macaca fuscata]	23	628	
gi 693787 gb AAB31269.1	tumor suppressor [Canis familiaris]	23	628	
gi 8400738 ref NP_000537.2	tumor protein p53 (Homo sapiens...	23	628	<b>L</b>
gi 4959058 gb AAD34216.1	AF071574.1 tumor suppressor protei...	23	628	

#### Alignments

Get selected sequences	Select all	Deselect all
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gi 21355617 ref NP_651115.1	<b>L</b> CG10873-PA [Drosophila melanogaster]
gi 7211767 gb AAF40427.1	AF224713.1 <b>L</b> transcription factor p53 [Drosophila melano]
gi 7211769 gb AAF40428.1	AF224714.1 <b>L</b> transcription factor p53 [Drosophila melano]
gi 7381624 gb AAF61572.1	AF244918.1 <b>L</b> p53 tumor suppressor-like protein [Drosophi]
gi 8272608 gb AAF74277.1	AF250918.1 <b>L</b> transcription factor [Drosophila melanogast
gi 8453176 gb AAF75270.1	AF263722.1 <b>L</b> transcription factor p53 [Drosophila melano]
gi 10726710 gb AAF56087.2	<b>L</b> CG10873-PA [Drosophila melanogaster]
gi 17861528 gb AAL39241.1	<b>L</b> GH11591P [Drosophila melanogaster]
gi 18032162 gb AAL56639.1	AF192555.1 p53-like regulator of apoptosis and cell cyc
melanogaster]	
Length = 385	

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 ICTCPKRD 9  
ICTCPKRD  
Sbjct: 260 ICTCPKRD 267

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[\[>gi|25009887|gb|AA071112.1\]](#) [\[L\]](#) AT28346p [Drosophila melanogaster]  
Length = 519

Score = 31.2 bits (66), Expect = 1.8  
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 ICTCPKRD 9  
ICTCPKRD  
Sbjct: 394 ICTCPKRD 401

[\[>gi|31207283|ref|XP\\_312608.1\]](#) [\[L\]](#) ENSANGP00000014785 [Anopheles gambiae]  
[gi|21295812|gb|EAA07957.1\]](#) ENSANGP00000014785 [Anopheles gambiae str. PEST]  
Length = 338

Score = 28.2 bits (59), Expect = 14  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 ICTCPKRD 9  
IC+CPKRD  
Sbjct: 310 ICSCPKRD 317

[\[>gi|3695096|gb|AAC62642.1\]](#) [\[L\]](#) DN p63 gamma [Mus musculus]  
Length = 389

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPKRD 257

[\[>gi|13751181|emb|CAC37102.1\]](#) [\[L\]](#) DN KBT gamma protein [Rattus norvegicus]  
Length = 393

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPKRD 257

[\[>gi|13751173|emb|CAC37098.1\]](#) [\[L\]](#) TAI KBT alpha protein [Rattus norvegicus]  
Length = 663

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 326 RICACPKRD 334

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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[\[>gi|20428532|gb|AAK81886.1\]](#) [\[L\]](#) DN p73 gamma [Homo sapiens]  
Length = 426

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 244 RICACPKRD 252

[\[>gi|1813455|gb|AAB41833.1\]](#) [\[L\]](#) p53  
Length = 238

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 166 RICACPKRD 174

[\[>gi|19909983|dbj|BAB87245.1\]](#) [\[L\]](#) deltan p73 beta [Homo sapiens]  
[gi|20428530|gb|AAK81885.1\]](#) [\[L\]](#) DN p73 beta [Homo sapiens]  
Length = 450

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 244 RICACPKRD 252

[\[>gi|7248451|gb|AAF43492.1\]](#) [\[L\]](#) p51 isoform delnbeta [Homo sapiens]  
Length = 461

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPKRD 257

[\[>gi|20892181|ref|XP\\_147232.1\]](#) [\[L\]](#) transfection related protein 63 [Mus musculus]  
Length = 465

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 128 RICACPRGD 136

>gi|3695094|gb|AAC62641.1| TA\*P63 alpha [Mus musculus]  
 Length = 680  
 Score = 25.2 bits (52), Expect = 108  
 Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 343 RICACPRGD 351

>gi|12060406|dbj|BAB20591.1| delta N p73L [Homo sapiens]  
 Length = 501  
 Score = 25.2 bits (52), Expect = 108  
 Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 164 RICACPRGD 172

>gi|4803651|emb|CAA72225.1| P73 splice variant [Cercopithecus aethiops]  
 Length = 499  
 Score = 25.2 bits (52), Expect = 108  
 Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 293 RICACPRGD 301

>gi|13751179|emb|CAC37101.1| TA2 KET gamma protein [Rattus norvegicus]  
 Length = 487  
 Score = 25.2 bits (52), Expect = 108  
 Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 343 RICACPRGD 351

>gi|15072750|emb|CAC48053.1| p63 delta [Homo sapiens]  
 Length = 232  
 Score = 25.2 bits (52), Expect = 108

Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 191 RICACPRGD 199

>gi|29470179|gb|AA074632.1| p73 [Danio rerio]  
 Length = 640  
 Score = 25.2 bits (52), Expect = 108  
 Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 300 RICACPRGD 308

>gi|2581764|gb|AA82420.1| p53 [Cricetulus griseus]  
 Length = 205  
 Score = 25.2 bits (52), Expect = 108  
 Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 148 RICACPRGD 156

>gi|8217484|emb|CAB92742.1| dJ1092A11.2 (tumor protein p73) [Homo sapiens]  
 Length = 661  
 Score = 25.2 bits (52), Expect = 108  
 Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 318 RICACPRGD 326

>gi|2370178|emb|CAA72221.1| second splice variant [Homo sapiens]  
 Length = 588  
 Score = 25.2 bits (52), Expect = 108  
 Identities = 7/9 (77%), Positives = 7/9 (77%)  
 Query: 1 RICTCPKRD 9  
 RIC CP RD  
 Sbjct: 245 RICACPRGD 253

>gi|21264484|sp|P79820|p53-ORF1A Cellular tumor antigen p53 (Tumor suppressor p;  
 gi|4101544|gb|AAD01195.1| tumor suppressor protein p53 [Oryzias latipes]

Length = 352  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 254 RICACPRGD 262

>gi|1184759|gb|AA87577.1| p53 tumor suppressor homolog  
Length = 189  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 89 RICACPRGD 97

>gi|1184757|gb|AA87576.1| p53 tumor suppressor homolog  
Length = 228  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 97 RICACPRGD 105

>gi|7248450|gb|AAF43491.1| p51 isoform delNalpha [Homo sapiens]  
Length = 586  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPRGD 257

>gi|7248447|gb|AAF43488.1| p51 isoform TP63beta [Homo sapiens]  
Length = 516  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 304 RICACPRGD 312

>gi|3273745|gb|AAC24830.1| p53 homolog [Homo sapiens]  
Length = 356  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPRGD 257

>gi|473579|gb|AB41344.1| tumor supressor p53 [Mesocricetus auratus]  
Length = 396  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 276 RICACPRGD 284

>gi|27527178|emb|CAD10682.1| p53 protein [Monodelphis domestica]  
Length = 258  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 145 RICACPRGD 153

>gi|12024746|gb|AA645609.1| TA p63 gamma [Homo sapiens]  
Length = 487  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 343 RICACPRGD 351

>gi|3695098|gb|AA662643.1| DN p63 beta [Mus musculus]  
Length = 461  
Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)  
Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPRGD 257

>gi|4689086|gb|AAD27752.1|AF043641.1 p73 [Barbus barbuis]  
Length = 641

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 301 RICACPGRD 309

>gi|6755883|ref|NP\_035771.1| L transformation related protein 63; KET protein; 1  
[Mus musculus]  
gi|3445482|dbj|BAA32432.1| L p73H [Mus musculus]  
gi|3695100|gb|AAC62644.1| L DN p63 alpha [Mus musculus]  
Length = 586

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPGRD 257

>gi|1244762|gb|AAA98563.1| p53 tumor suppressor homolog  
Length = 564

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 298 RICACPGRD 306

>gi|13751187|emb|CAC37105.1| L DN KET beta protein [Rattus norvegicus]  
Length = 461

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPGRD 257

>gi|13751175|emb|CAC37099.1| L DN KET alpha protein [Rattus norvegicus]  
Length = 586

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPGRD 257

>gi|23308709|ref|NP\_694518.1| L deltaNp63 isoform alpha 1; tumor protein p63 [D.  
gi|22652331|gb|AA03690.1|AF412283.1 L DN p63 alpha 1 [Danio rerio]  
Length = 588

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 247 RICACPGRD 255

>gi|26339452|dbj|BAC33397.1| unnamed protein product [Mus musculus]  
Length = 284

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPGRD 257

>gi|23308711|ref|NP\_694519.1| L deltaNp63 isoform gamma; tumor protein p63 [Danio  
gi|22652335|gb|AA03692.1|AF412285.1 L DN p63 gamma [Danio rerio]  
Length = 457

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 247 RICACPGRD 255

>gi|3695082|gb|AAC62635.1| L vA p63 alpha (Homo sapiens)  
Length = 641

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 304 RICACPGRD 312

>gi|1698502|gb|AAC60146.1| p53 [Oryzias latipes]

gi|12082495|gb|AAC48557.1|AF212997\_1 p53 tumor suppressor [Oryzias latipes]  
Length = 351

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 253 RICACPGRD 261

>gi|20850793|ref|XP\_131858.1| L transformation related protein 73 [Mus musculus]  
gi|30794514|ref|NP\_035772.1| L transformation related protein 73 [Mus musculus]  
gi|15209244|emb|CA881953.1| L P73 alpha protein [Mus musculus]  
Length = 631

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 285 RICACPGRD 293

>gi|13195250|gb|AAK15622.1|AF314148\_1 p63 DNA binding protein [Xenopus laevis]  
Length = 365

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPGRD 257

>gi|3510328|dbj|BAA32592.1| L p51A [Homo sapiens]  
gi|3695078|gb|AAC62633.1| L TA p63 gamma [Homo sapiens]  
gi|7248445|gb|AAF43486.1| p51 isoform TAp63gamma [Homo sapiens]  
Length = 448

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 304 RICACPGRD 312

>gi|13751185|emb|CAC37104.1| L TAI KET beta protein [Rattus norvegicus]  
Length = 538

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 326 RICACPGRD 334

>gi|451931|gb|AAA37086.1| tumor suppressor protein [Mesocricetus auratus]  
Length = 206

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 148 RICACPGRD 156

>gi|1813453|gb|AAB41832.1| p53  
Length = 286

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 166 RICACPGRD 174

>gi|3695080|gb|AAC62634.1| L DN p63 gamma [Homo sapiens]  
gi|7248449|gb|AAF43490.1| p51 isoform delNgamma [Homo sapiens]  
gi|12024749|gb|AAG45612.1| DN p63 gamma [Homo sapiens]  
Length = 393

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 249 RICACPGRD 257

>gi|1813451|gb|AAB41831.1| p53  
Length = 378

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 258 RICACPGRD 266

>gi|3970717|emb|CAA76562.1| L KET protein [Homo sapiens]  
Length = 680

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 343 RICACPRGD 351

>gi|23308685|ref|NP\_689454.1| deltanp63 isoform alpha 2; tumor protein p63 [D  
gi|21326973|gb|AA048108.1|AF487944.1 deltan p63 alpha [Danio rerio]  
gi|22652333|gb|AA03691.1|AF412284.1 DN p63 alpha 2 [Danio rerio]  
Length = 576

Score = 25.2 bits (52), Expect = 108  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9  
RIC CP RD  
Sbjct: 247 RICACPRGD 255

Get selected sequences Select all Deselect all

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
Posted date: Jul 10, 2003 1:49 AM  
Number of letters in database: 474,244,320  
Number of sequences in database: 1,477,204

Lambda K H  
0.354 0.293 2.12

Gapped  
Lambda K H  
0.294 0.110 0.610

Matrix: PAM30  
Gap Penalties: Existence: 9, Extension: 1  
Number of Hits to DB: 7,525,701  
Number of Sequences: 1477204  
Number of extensions: 33882  
Number of successful extensions: 2403  
Number of sequences better than 20000.0: 100  
Number of HSP's better than 20000.0 without gapping: 2193  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 2403  
length of query: 9  
length of database: 474,244,320  
effective HSP length: 0  
effective length of query: 9  
effective length of database: 474,244,320

effective search space: 4268198880  
effective search space used: 4268198880  
T: 11  
A: 40  
X1: 14 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 35 (19.6 bits)  
S2: 35 (18.0 bits)

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057869726-06677-18835

Query= SEQID29  
(9 letters)

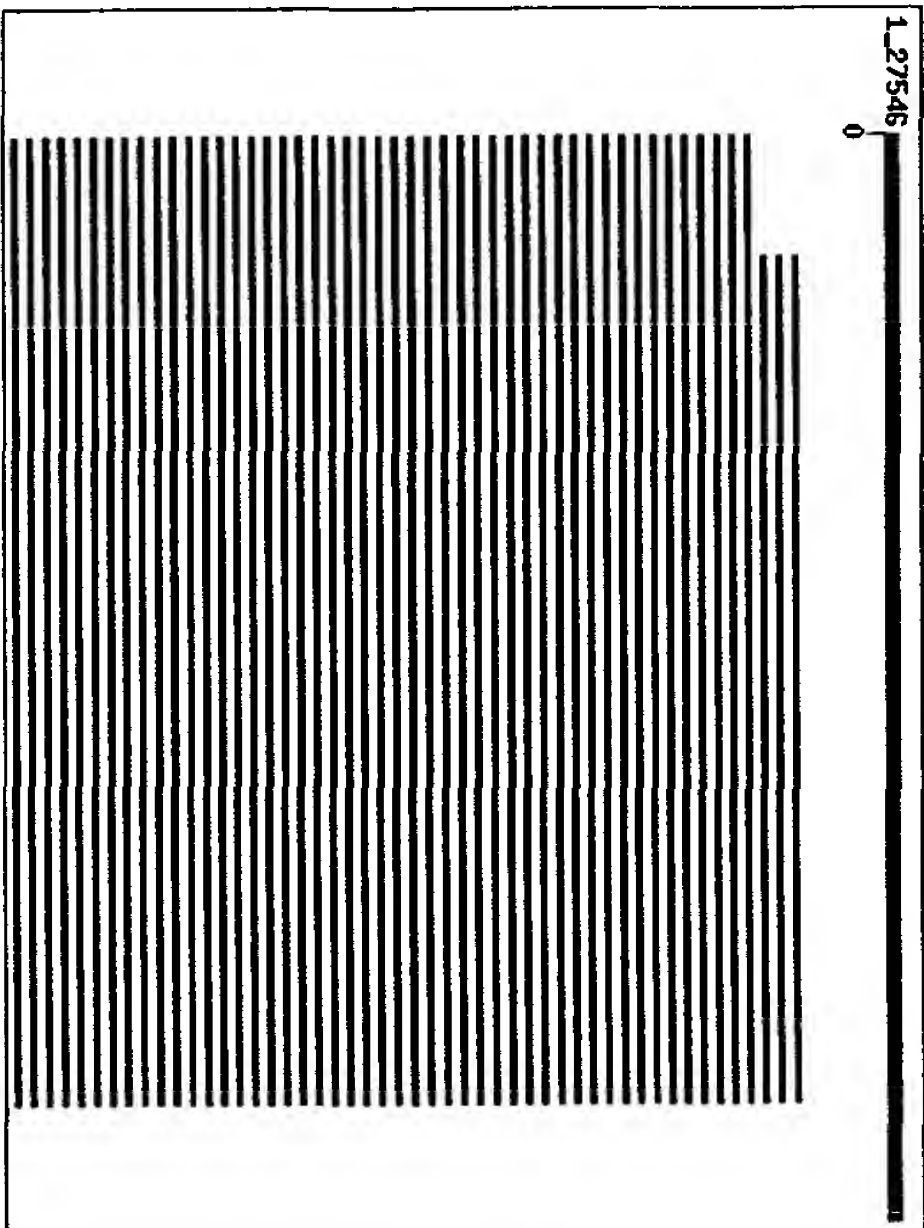
Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

Distribution of 101 Blast Hits on the Query Sequence

[Mouse-over to show define and scores. Click to show alignments](#)



Related Structures

Sequences producing significant alignments:

	Score	E
(bits)	Value	
gi 21355617 ref NP_651115.1	29	10
gi 25009887 gb AAAT71112.1	29	10
gi 31207283 ref XP_312608.1	26	80
gi 129372 sp P10361 P53_RAT	25	144
gi 7259331 dbj BA92786.1	25	144
gi 693787 gb AAB31269.1	25	144
gi 8400738 ref NP_000537.2	25	144
gi 4959058 gb AAD34216.1 AF071574.1	25	144
gi 1709531 sp P51664 P53_SHEEP	25	144
gi 129369 sp P04637 P53_HUMAN	25	144
gi 1836145 gb AAB46899.1	25	144
gi 11321107 gb AAG34052.1	25	144
gi 16266760 dbj BAB69969.1	25	144
gi 21730310 pdb 1GZHI C	25	144
gi 6755881 ref NP_035770.1	25	144
gi 200201 gb AA39882.1	25	144
gi 1154648 emb CAA62905.1	25	144
gi 2811079 sp O12946 P53_PLAFA	25	144
gi 1171969 sp P41685 P53_FELCA	25	144
gi 1000577 gb AAB42022.1	25	144
gi 975651 emb CAA62450.1	25	144
gi 20900490 ref XP_128695.1	25	144
gi 8698976 gb AAF78535.1 AF223795.1	25	144



gi 1729419 dbj BA08629.1	p53 gene product (Bos primigenius)	25	144	
gi 4731632 gb AAD28535.1	AF135121.1 tumor suppressor protei...	25	144	<b>L</b>
gi 10720195 sp Q9W678 P53	BARBU Cellular tumor antigen p53 ...	25	144	
gi 223827 prf 1001197A	antigen p53, tumor	25	144	
gi 11342599 emb CAC17147.1	transformation related protein ...	25	144	<b>L</b>
gi 18859503 ref NP_571402.1	tumor protein p53; tumor suppr...	25	144	<b>L</b>
gi 10720186 sp Q9TUB2 P53	PIG Cellular tumor antigen p53 (T...	25	144	
gi 2829194 gb AAC26190.1	tumor suppressor ortholog [Xiphop...	25	144	
gi 4996230 dbj BAA78379.1	p53 (Canis familiaris)	25	144	
gi 13591878 ref NP_112251.1	tumor protein p53; tumor prote...	25	144	<b>L</b>
gi 129374 sp P07193 P53	XENLA Cellular tumor antigen p53 (T...	25	144	
gi 506453 emb CAA42635.1	p53 transformation suppressor (Ho...	25	144	<b>L</b>
gi 5353744 gb AAD42225.1	p53 protein (Canis familiaris)	25	144	
gi 1389675 gb BAB18936.1	tumor-suppressor (Equus caballus)	25	144	
gi 2961247 gb AAC05704.1	tumor suppressor p53 (Mus musculus)	25	144	<b>L</b>
gi 15375072 gb AAK94783.1	transformation related protein 5...	25	144	<b>L</b>
gi 8698972 gb AAF78533.1	AF223793.1 tumor suppressor p53 (On...	25	144	
gi 28975327 gb AAO60156.1	tumor suppressor p53; p53as (Mus...	25	144	<b>L</b>
gi 49590562 gb AAD34215.1	AF071573.1 tumor suppressor protei...	25	144	
gi 6841071 gb AAF28891.1	AF124298.1 p53 protein (Sus scrofa)	25	144	
gi 53571 emb CAA25323.1	p53 (Mus musculus)	25	144	<b>L</b>
gi 18997087 gb AAL83290.1	AF475081.1 P53 (Delphinapterus le...	25	144	
gi 14039818 gb AAK53397.1	AF367373.1 p53 tumor suppressor (...)	25	144	
gi 28849929 ref NP_776626.1	p53 tumor suppressor phosphopr...	25	144	<b>L</b>
gi 3024331 sp P56423 P53	MACPA Cellular tumor antigen p53 (...)	25	144	<b>S</b>
gi 2781308 pdb 1YCS A	Chain A, p53-53bp2 Complex	25	144	
gi 642241 emb CAA25652.1	p53 (Homo sapiens)	25	144	<b>L</b>
gi 10720196 sp Q9W679 P53	TEXTU Cellular tumor antigen p53 ...	25	144	
gi 10720197 sp Q9WUR6 P53	CAVPO Cellular tumor antigen p53 ...	25	144	
gi 506449 emb CAA42633.1	p53 transformation suppressor (Ho...	25	144	<b>L</b>
gi 129368 sp P10360 P53	CHICK Cellular tumor antigen p53 (T...	25	144	
gi 1619833 gb BAB16961.1	p53 (Canis familiaris)	25	144	
gi 14719450 pdb 1HU8 A	Chain A, Crystal Structure Of The Mo...	25	144	<b>S</b>
gi 506445 emb CAA42631.1	p53 transformation suppressor (Ho...	25	144	<b>L</b>
gi 5081783 gb AAD39535.1	AF151353.1 tumor suppressor p53 (M...	25	144	<b>L</b>
gi 10720190 sp Q30006 P53	MARMO Cellular tumor antigen p53 ...	25	144	
gi 1223855 gb AAA92052.1	p53 (Xiphophorus maculatus)	25	144	
gi 506443 emb CAA42630.1	p53 transformation suppressor (Ho...	25	144	<b>L</b>
gi 21730308 pdb 1GZH A	Chain A, Crystal Structure Of The Br...	25	144	<b>S</b>
gi 339814 gb AAA61211.1	p53 antigen	25	144	<b>L</b>
gi 2842741 sp Q95330 P53	RABIT Cellular tumor antigen p53 (...)	25	144	
gi 1753089 gb BAB39322.1	Cellular phosphoprotein p53	25	144	
gi 339816 gb AAA61212.1	p53 antigen	25	144	<b>L</b>
gi 10720193 sp Q92143 P53	XIPMA Cellular tumor antigen p53 ...	25	144	
gi 506441 emb CAA42629.1	p53 transformation suppressor (Ho...	25	144	<b>L</b>
gi 6093639 sp Q29537 P53	CANPA Cellular tumor antigen p53 (...)	25	144	
gi 10720192 sp Q93379 P53	ICTFU Cellular tumor antigen p53 ...	25	144	
gi 1463021 gb AAC37335.1	p53 (Canis familiaris)	25	144	
gi 481535 pir S38824	cellular tumor antigen p53, minor spl...	25	144	<b>L</b>
gi 386994 gb AAA59987.1	phosphoprotein p53 (Homo sapiens)	25	144	<b>L</b>
gi 545102 gb AAC60746.1	p53 (Xenopus laevis)	25	144	
gi 10720191 sp Q57538 P53	XIPHE Cellular tumor antigen p53 ...	25	144	

gi 20151154 pdb 1KZY A	Chain A, Crystal Structure Of The 53...	25	144	<b>S</b>
gi 3024332 sp P56424 P53	MACMU Cellular tumor antigen p53 (...)	25	144	
gi 1310770 pdb 1TSR A	Chain A, p53 Core Domain In Complex W...	25	144	<b>S</b>
gi 1938365 gb BAB80959.1	mutant p53 (Rattus norvegicus)	25	144	<b>L</b>
gi 506439 emb CAA42628.1	p53 transformation suppressor (Ho...	25	144	<b>L</b>
gi 129367 sp P13481 P53	CERAB Cellular tumor antigen p53 (T...	25	144	
gi 506451 emb CAA42634.1	p53 transformation suppressor (Ho...	25	144	<b>L</b>
gi 129372 sp P02340 P53	MUSE Cellular tumor antigen p53 (T...	25	144	<b>L</b>
gi 129373 sp P25035 P53	ONCMY Cellular tumor antigen p53 (T...	25	144	
gi 468514 emb CAA54672.1	p53 (Xenopus laevis)	25	144	
gi 29468129 gb AAO85406.1	AF365873.1 tumor suppressor p53 (...)	25	144	<b>L</b>
gi 4959054 gb AAD34214.1	AF071572.1 tumor suppressor protei...	25	144	
gi 26348179 dbj BAC37729.1	unnamed protein product (Mus mu...	25	144	<b>L</b>
gi 575528 dbj BAA03927.1	p53 protein (Felis catus)	25	144	
gi 2465420 gb BAB72093.1	chimeric tumour suppressor (synth...	25	144	
gi 2833362 sp Q29480 P53	BOUAS Cellular tumor antigen p53 (...)	25	144	
gi 2829679 sp P79892 P53	HORSE Cellular tumor antigen p53 (...)	25	144	
gi 2842672 sp Q64662 P53	SPERB Cellular tumor antigen p53 (...)	25	144	
gi 506435 emb CAA42626.1	p53 transformation suppressor (Ho...	25	144	<b>L</b>
gi 20521856 dbj BAA13377.2	K1AA0246 protein (Homo sapiens)	24	194	
gi 2279437 dbj BAC15606.1	FRBE-1 (Homo sapiens)	24	194	<b>L</b>
gi 20149762 ref NP_619613.1	stabilin 1; stabilin-1; stabil...	24	194	<b>L</b>
gi 12225240 ref NP_055991.1	stabilin 1 (Homo sapiens) >gi ...	24	194	<b>L</b>
gi 26329891 dbj BAC28684.1	unnamed protein product (Mus mu...	24	194	
gi 13626617 sp Q9TV36 FBN1	PIG Fibrillin 1 precursor >gi 57...	24	260	

# Alignments

Get selected sequences

Select all

Deselect all

>gi 21355617 ref NP_651115.1	CG10873-PA (Drosophila melanogaster)	
gi 7211767 gb AAF40427.1	AF224713.1 transcription factor p53 (Drosophila melano	
gi 7211769 gb AAF40428.1	AF224714.1 transcription factor p53 (Drosophila melano	
gi 7381624 gb AAF61572.1	AF244918.1 p53 tumor suppressor-like protein (Drosophi	
gi 8272608 gb AAF74277.1	AF250918.1 transcription factor [Drosophila melanogast	
gi 8453176 gb AAF75270.1	AF263722.1 transcription factor p53 (Drosophila melano	
gi 10726710 gb AAF56087.2	CG10873-PA (Drosophila melanogaster)	
gi 17861528 gb AAF39241.1	GHI1591P (Drosophila melanogaster)	
gi 18032162 gb AAF56639.1	AF192555.1 p53-like regulator of apoptosis and cell cyc	
melanogaster)		
Length = 385		

Score = 28.6 bits (60), Expect = 10  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 VCPCPKRD 9  
+CTCPCPKRD  
Sbjct: 260 ICTCPCPKRD 267

```

>gi|25009887|gb|AA071112.1| AT28346p [Drosophila melanogaster]
Length = 519
Score = 28.6 bits (60), Expect = 10
Identities = 7/8 (87%), Positives = 8/8 (100%)
Query: 2 VCTCPKRD 9
+CTCPKRD
Sbjct: 394 ICTCPKRD 401

>gi|31207283|ref|XP_312608.1| ENSANGP00000014785 [Anopheles gambiae]
gi|21295812|gb|EA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PSTV]
Length = 338
Score = 25.7 bits (53), Expect = 80
Identities = 6/8 (75%), Positives = 8/8 (100%)
Query: 2 VCTCPKRD 9
+C+CPKRD
Sbjct: 310 ICSCPKRD 317

>gi|129372|sp|P10361|p53_RAT Cellular tumor antigen p53 (Tumor suppressor p53)
gi|32070|pir|S02192 cellular tumor antigen p53 - rat
gi|56829|emb|CA31457.1| L nuclear protein p53 (AA 1 - 391) [Rattus norvegicus]
Length = 391
Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 271 RVCACPGRD 279

>gi|7259331|dbj|BAA92786.1| p53 [Macaca fuscata]
Length = 181
Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 148 RVCACPGRD 156

>gi|693787|gb|AA01269.1| tumour suppressor [Canis familiaris]
Length = 32
Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

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```

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 4 RVCACPGRD 12

>gi|8400738|ref|NP_000537.2| L tumor protein p53 [Homo sapiens]
gi|625300|pir|DNU03 cellular tumor antigen p53 [validated] - human
gi|35214|emb|CAA38095.1| L protein p53 [Homo sapiens]
gi|506437|emb|CAA42627.1| L p53 transformation suppressor [Homo sapiens]
gi|3041867|gb|AAC12971.1| L p53 [Homo sapiens]
gi|4732147|gb|AAD28628.1|AF136271.1 L tumor suppressor protein p53 [Homo sapiens]
gi|11066970|gb|AA028785.1|AF307851.1 L p53 protein [Homo sapiens]
Length = 393
Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 273 RVCACPGRD 281

>gi|4959058|gb|AAD34216.1|AF071574.1 tumor suppressor protein p53 [Oncomorphus]
Length = 265
Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 252 RVCACPGRD 260

>gi|1709531|sp|P51664|p53_SHEEP Cellular tumor antigen p53 (Tumor suppressor p5)
gi|602357|emb|CAA57349.1| p53 [Ovis aries]
Length = 382
Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 262 RVCACPGRD 270

>gi|129369|sp|P04637|p53_HUMAN L Cellular tumor antigen p53 (Tumor suppressor p)
p53) (Antigen NY-CO-13)
gi|35210|emb|CAA26306.1| L p53 tumor antigen (aa 1-7) [Homo sapiens]
gi|189476|gb|AA059988.1| L phosphoprotein p53
gi|7595312|gb|AA064408.1|AF192534.1 tumor suppressor protein p53 [Expression vect]
Length = 393

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Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|1836145|gb|AAB46899.1| sequence-specific transcription factor [Equidae]  
Length = 263

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 224 RVCACPGRD 232

>gi|11321107|gb|AAG34052.1| p53 tumor suppressor [Rattus norvegicus]  
Length = 53

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 12 RVCACPGRD 20

>gi|16266760|dbj|BAB69969.1| p53 [Meriones unguiculatus]  
Length = 390

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 271 RVCACPGRD 279

>gi|21730310|pdb|1GZH|C 5 Chain C, Crystal Structure Of The Brct Domains Of Hum  
To The P53 Tumor Suppressor  
Length = 198

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 179 RVCACPGRD 187

>gi|6755881|ref|NP\_035770.1| 5 transformation related protein 53 [Mus musculus]  
gi|53576|emb|CAA25625.1| 5 p53 polypeptide (aa 1-390) [Mus musculus]  
gi|871421|emb|CAA25420.1| 5 cellular tumour antigen p53 [Mus musculus]  
Length = 390

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|200201|gb|AA39882.1| 5 p53  
Length = 390

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|1154648|emb|CAA62905.1| p53 [Equus caballus]  
Length = 196

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 140 RVCACPGRD 148

>gi|2811079|sp|O12946|P53\_PLAFE Cellular tumor antigen p53 (Tumor suppressor p53;  
gi|1922902|emb|CAA70123.1| p53 [Platichthys flesus]  
Length = 366

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 248 RVCACPGRD 256

>gi|1171969|sp|P41685|P53\_FELCA Cellular tumor antigen p53 (Tumor suppressor p53;  
gi|538225|dbj|BA05653.1| p53 [Felis catus]  
Length = 386

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9  
RVC CP RD  
Sbjct: 266 RVCACPGRD 274

>gi|1000577|gb|AAB42022.1| p53 [Canis familiaris]  
length = 276

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9  
RVC CP RD  
Sbjct: 237 RVCACPGRD 245

>gi|975651|emb|CAA62450.1| p53 [Callionymus lyra]  
length = 45

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9  
RVC CP RD  
Sbjct: 37 RVCACPGRD 45

>gi|20900490|ref|XP\_128695.1| similar to transformation related protein 53 [M  
length = 151

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9  
RVC CP RD  
Sbjct: 114 RVCACPGRD 122

>gi|8698976|gb|AAF78535.1|AF223795.1 tumor suppressor p53 [Oncothynchus tshawytsch  
gi|8698978|gb|AAF78536.1|AF223796.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698980|gb|AAF78537.1|AF223797.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698982|gb|AAF78538.1|AF223798.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698984|gb|AAF78539.1|AF223799.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698986|gb|AAF78540.1|AF223800.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698988|gb|AAF78541.1|AF223801.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698990|gb|AAF78542.1|AF223802.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698992|gb|AAF78543.1|AF223803.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698994|gb|AAF78544.1|AF223804.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698996|gb|AAF78545.1|AF223805.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8698998|gb|AAF78546.1|AF223806.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699000|gb|AAF78547.1|AF223807.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699002|gb|AAF78548.1|AF223808.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699004|gb|AAF78549.1|AF223809.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699006|gb|AAF78550.1|AF223810.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699008|gb|AAF78551.1|AF223811.1 tumor suppressor p53 [Oncothynchus tshawytscha

gi|8699010|gb|AAF78552.1|AF223812.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699012|gb|AAF78553.1|AF223813.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699014|gb|AAF78554.1|AF223814.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699016|gb|AAF78555.1|AF223815.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699018|gb|AAF78556.1|AF223816.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699020|gb|AAF78557.1|AF223817.1 tumor suppressor p53 [Oncothynchus tshawytscha  
gi|8699022|gb|AAF78558.1|AF223818.1 tumor suppressor p53 [Oncothynchus tshawytscha  
length = 146

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9  
RVC CP RD  
Sbjct: 42 RVCACPGRD 50

>gi|1729419|dbj|BA008629.1| p53 gene product [Bos primigenius]  
length = 374

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9  
RVC CP RD  
Sbjct: 254 RVCACPGRD 262

>gi|4731632|gb|AAD28535.1|AF135121.1 tumor suppressor protein p53 [Homo sapien  
length = 393

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9  
RVC CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|10720195|sp|Q9W678|P53\_BARBU Cellular tumor antigen p53 [Tumor suppressor p:  
gi|4959050|gb|AAD34212.1|AF071570.1 tumor suppressor protein p53 [Barbus barbus]  
length = 369

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9  
RVC CP RD  
Sbjct: 237 RVCACPGRD 245

>gi|223827|ref|1001197A antigen p53, tumor  
length = 390  
Score = 24.8 bits (51), Expect = 144

Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|11342592|emb|CAC17147.1| **L** transformation related protein 53 (Mus musculus)  
Length = 307

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|18859503|ref|NP\_571402.1| **L** tumor protein p53; tumor suppressor homolog p53;  
antigen p53 (Danio rerio)  
gi|2829677|sp|P79734|P53\_BRAE Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|1778019|gb|AAB40617.1| **L** tumor suppressor p53 (Danio rerio)  
Length = 373

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 241 RVCACPGRD 249

>gi|10720186|sp|Q9TUB2|P53\_PIG Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|6165623|gb|AAF04620.1|AF098067.1 tumor suppressor p53 (Sus scrofa)  
Length = 386

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 266 RVCACPGRD 274

>gi|2829194|gb|AAC26190.1| tumor suppressor ortholog (Xiphophorus maculatus)  
Length = 153

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 47 RVCACPGRD 55

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|4996230|dbj|BAA78379.1| P53 (Canis familiaris)  
Length = 381

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 261 RVCACPGRD 269

>gi|13591878|ref|NP\_112251.1| **L** tumor protein p53; tumor protein p53 (Li-Fraumeni  
syndrome)  
gi|205952|gb|AAA41788.1| **L** tumor suppressor  
Length = 391

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 271 RVCACPGRD 279

>gi|129374|sp|P07193|P53\_XENLA Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|85718|pir|A29376 cellular tumor antigen p53 - African clawed frog  
gi|64962|emb|CAA28821.1 ORF (AA 1-363) (Xenopus laevis)  
gi|214640|gb|AAA49923.1 p53 protein homologue; putative  
Length = 363

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 248 RVCACPGRD 256

>gi|506453|emb|CAA42635.1| **L** p53 transformation suppressor (Homo sapiens)  
Length = 393

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|5353744|gb|AAD42225.1| p53 protein (Canis familiaris)  
Length = 246

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 156 RVCACPGRD 164

>gi|1389675|gb|AA018936.1| tumor-suppressor [Equus caballus]  
Length = 205

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 149 RVCACPGRD 157

>gi|2961247|gb|AAC05704.1| tumor suppressor p53 [Mus musculus]  
Length = 390

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|15375072|gb|AA094783.1| transformation related protein 53 [Mus musculus]  
Length = 391

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|8698972|gb|AA078533.1|AF223793.1 tumor suppressor p53 [Oncorhynchus mykiss]  
gi|8698974|gb|AA078534.1|AF223794.1 tumor suppressor p53 [Oncorhynchus mykiss]  
Length = 146

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 42 RVCACPGRD 50

>gi|28975327|gb|AA060156.1| tumor suppressor p53; p53as [Mus musculus]  
Length = 381

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 270 RVCACPGRD 278

>gi|4959056|gb|AAD34215.1|AF071573.1 tumor suppressor protein p53 [Oncorhynchus]  
Length = 265

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 252 RVCACPGRD 260

>gi|6841071|gb|AA028891.1|AF124298.1 p53 protein [Sus scrofa]  
Length = 387

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 262 RVCACPGRD 270

>gi|53571|emb|CA025323.1| p53 [Mus musculus]  
Length = 389

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 269 RVCACPGRD 277

>gi|18997097|gb|AA183290.1|AF475081.1 p53 [Delphinapterus leucas]  
Length = 387

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 267 RVCACPGRD 275



>gi|14039818|gb|AAK53397.1|AF367373.1 p53 tumor suppressor [Mus musculus]  
Length = 207

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 148 RVCACPGRD 156

>gi|28849929|ref|NP\_776626.1| p53 tumor suppressor phosphoprotein [Bos taurus]  
gi|2499426|sp|Q29628|P53\_BOVIN Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|1083096|pir|S51648 cellular tumor antigen p53 - bovine  
gi|602333|emb|CAA57348.1| p53 [Bos taurus]  
gi|1916676|gb|AAB51214.1| 53 kDa phosphoprotein [Bos indicus]  
Length = 386

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 266 RVCACPGRD 274

>gi|3024331|sp|P56423|P53\_MACFA Cellular tumor antigen p53 (Tumor suppressor p53)  
gi|2689467|gb|AAB91535.1| p53 [Macaca fascicularis]  
Length = 393

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 273 RVCACPGRD 281

>gi|2781308|pdb|1XCS|A S Chain A, p53-53bp2 Complex  
Length = 199

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 180 RVCACPGRD 188

>gi|642241|emb|CAJ25652.1| p53 [Homo sapiens]  
Length = 293

Score = 24.8 bits (51), Expect = 144  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9  
RVC CP RD  
Sbjct: 173 RVCACPGRD 181

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS  
translations:PDB+SwissProt+PIR+PRF  
Posted date: Jul 10, 2003 1:49 AM  
Number of letters in database: 474,244,320  
Number of sequences in database: 1,477,204

Lambda K H  
0.357 0.295 2.13

Gapped K H  
Lambda 0.294 0.110 0.610

Matrix: PAM30  
Gap Penalties: Existence: 9, Extension: 1  
Number of Hits to DB: 7,701,129  
Number of Sequences: 1477204  
Number of extensions: 39535  
Number of successful extensions: 1949  
Number of sequences better than 20000.0: 100  
Number of HSP's better than 20000.0 without gapping: 1769  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1949  
length of query: 9  
length of database: 474,244,320  
effective HSP length: 0  
effective length of query: 9  
effective length of database: 474,244,320  
effective search space: 4268198880  
effective search space used: 4268198880  
T: 11  
A: 40  
X1: 14 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 35 (19.8 bits)  
S2: 35 (18.0 bits)



NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057870092-013883-18202

Query= SEQID30 (9 letters)

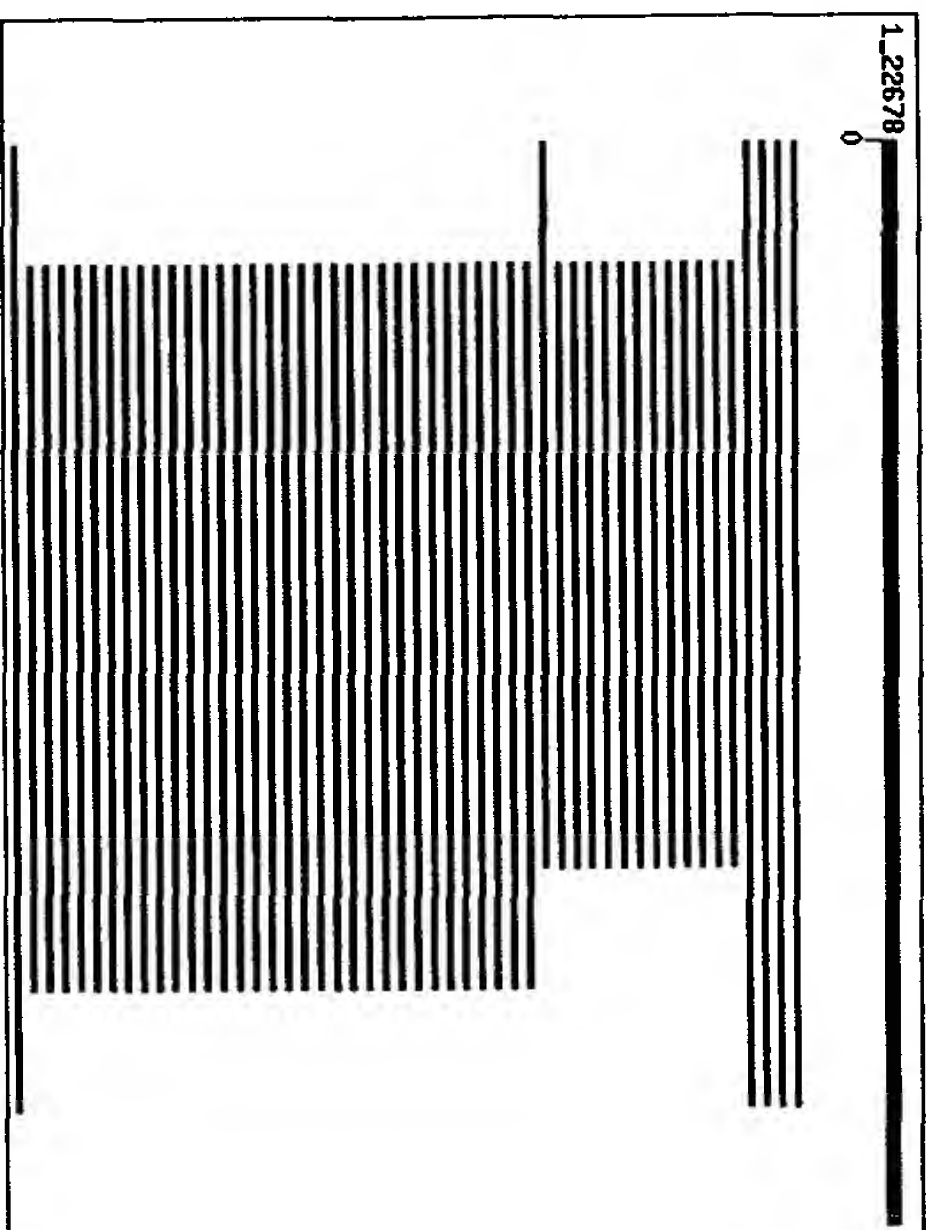
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF 1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQ

Taxonomy reports

Distribution of 125 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:

	Score	E
(bits) value		
gi 21355617 ref NP_651115.1  CG10873-PA [Drosophila melanogaster]	32	1.3
gi 25009887 gb AAW71112.1  AT28346P [Drosophila melanogaster]	32	1.3
gi 31207283 ref XP_312608.1  ENSMANGP00000014785 [Anopheles ...]	29	10
gi 18150104 dbj BAB83667.1  insulin receptor [Paralichthys ...]	24	194
gi 13626617 sp O9TV36 FBN1_PIG Fibrillin 1 precursor >gi 57...	24	260
gi 3688648 gb AAC62317.1  mutant fibrillin-1 [Mus musculus]	24	260
gi 642072 gb AA61825.1  fibrillin-1	24	260
gi 13929178 ref NP_114013.1  fibrillin-1 [Rattus norvegicus...]	24	260
gi 24430141 ref NP_000129.2  fibrillin 1 [Homo sapiens]	24	260
gi 7459676 pic A47221 fibrillin 1 precursor - human (fragm...	24	260
gi 2494284 sp O61554 FBN1_MOUSE Fibrillin 1 precursor >gi 1...	24	260
gi 6679759 ref NP_032019.1  fibrillin 1; tight skin [Mus mu...	24	260
gi 27806637 ref NP_776478.1  fibrillin 1 [Bos taurus] >gi 1...	24	260
gi 28487571 ref XP_192917.2  fibrillin 1 [Mus musculus]	24	260
gi 544279 sp P35555 FBN1_HUMAN Fibrillin 1 precursor >gi 30...	24	260
gi 1335064 emb CAA45118.1  fibrillin [Homo sapiens]	24	260
gi 729929 sp P80424 DPTI_HIRME Leech-derived tryptase inhib...	24	349
gi 16506777 gb AA123943.1 AF425233.5 putative aldehyde dehy...	23	628
gi 21229579 ref NP_635496.1  chloroacetaldehyde dehydrogena...	23	628
gi 17988030 ref NP_540664.1  ALDEHYDE DEHYDROGENASE [Brucel...	23	628
gi 9652162 gb AAFP91420.1 AF277380.1 aldehyde dehydrogenase ...	23	628
gi 23015854 ref ZP_00055619.1  hypothetical protein [Magnet...	23	628

gi 15597180 ref NP_250674.1	probable aldehyde dehydrogenas...	23	628
gi 28867956 ref NP_790575.1	aldehyde dehydrogenase family ...	23	628
gi 23308979 ref NP_601988.2	NAD-dependent aldehyde dehydro...	23	628
gi 23099988 ref NP_693455.1	aldehyde dehydrogenase [Oceano...	23	628
gi 15660836 ref NP_230467.1	aldehyde dehydrogenase [Vibrio...	23	628
gi 2660726 gb AAC13644.1	NAD-dependent chloroacetaldehyde...	23	628
gi 23062064 ref NP_00086869.1	hypothetical protein [Pseudo...	23	628
gi 15613244 ref NP_24547.1	aldehyde dehydrogenase [Bacill...	23	628
gi 15593281 gb AA02234.1 AF414083_5	putative truncated ald...	23	628
gi 30065134 ref NP_839305.1	aldehyde dehydrogenase B [lact...	23	628
gi 13475541 ref NP_107105.1	aldehyde dehydrogenase [Mesorh...	23	628
gi 26989399 ref NP_744824.1	aldehyde dehydrogenase family ...	23	628
gi 29833739 ref NP_828353.1	putative aldehyde dehydrogenas...	23	628
gi 17936107 ref NP_532897.1	aldehyde dehydrogenase [Agroba...	23	628
gi 15283977 gb AAK28545.2	putative aldehyde dehydrogenase ...	23	628
gi 15966104 ref NP_386457.1	PROBABLY ALDEHYDE DEHYDROGENAS...	23	628
gi 27468995 ref NP_765622.1	glycine betaine aldehyde dehyd...	23	628
gi 15889500 ref NP_355181.1	AGR_C_404ip [Agrobacterium tum...	23	628
gi 24375958 ref NP_720001.1	aldehyde dehydrogenase [Shewan...	23	628
gi 24114856 ref NP_709366.1	aldehyde dehydrogenase B [lact...	23	628
gi 16132093 gb AAU14969.1 AF418982_6	putative aldehyde dehy...	23	628
gi 39286801 gb AAC79659.1	NAD+ dependent acetaldehyde dehyd...	23	628
gi 4519175 gb BAA75508.1	aldehyde dehydrogenase [petroleu...	23	628
gi 27379895 ref NP_771424.1	aldehyde dehydrogenase [Bradyr...	23	628
gi 23469955 ref NP_00125289.1	hypothetical protein [Pseudo...	23	628
gi 21219685 ref NP_625464.1	aldehyde dehydrogenase [Strept...	23	628
gi 15825005 gb AAL09566.1 AF367720_1	lipoprotein receptor-r...	23	628
gi 23008217 ref NP_00049754.1	hypothetical protein [Magnet...	23	628
gi 15076881 gb AAK82977.1	NAD+-dependent aldehyde dehydrog...	23	628
gi 15641821 ref NP_231453.1	aldehyde dehydrogenase [Vibrio...	23	628
gi 15607599 ref NP_214972.1	hypothetical protein Rv0458 [M...	23	628
gi 25029181 ref NP_739235.1	putative aldehyde dehydrogenas...	23	628
gi 26968001 gb BAA24014.1	aldehyde dehydrogenase [Alteromo...	23	628
gi 26250230 ref NP_756270.1	aldehyde dehydrogenase B [Psch...	23	628
gi 32039193 ref NP_00137465.1	hypothetical protein [Pseudo...	23	628
gi 47586861 ref NP_002323.1	low density lipoprotein-related...	23	628
gi 15808007 ref NP_285671.1	aldehyde dehydrogenase [Deinoc...	23	628
gi 16127810 ref NP_422374.1	aldehyde dehydrogenase B [Caul...	23	628
gi 26987283 ref NP_742708.1	aldehyde dehydrogenase family ...	23	628
gi 16131459 ref NP_418045.1	aldehyde dehydrogenase B [lact...	23	628
gi 66787201 ref NP_032538.1	low density lipoprotein recepto...	23	628
gi 28898477 ref NP_798082.1	aldehyde dehydrogenase [Vibrio...	23	628
gi 1185011 sp P23240 DHAL_VIBCH	aldehyde dehydrogenase >gi 7...	23	628
gi 27367274 ref NP_762801.1	NAD-dependent aldehyde dehydro...	23	628
gi 15804128 ref NP_290167.1	aldehyde dehydrogenase B [lact...	23	628
gi 32042073 ref NP_00139656.1	hypothetical protein [Pseudo...	23	628
gi 11683071 sp P46368 DHA2_ALCEU	Acetaldehyde dehydrogenase ...	23	628
gi 23501111 ref NP_697238.1	aldehyde dehydrogenase family ...	23	628
gi 16762629 ref NP_458246.1	aldehyde dehydrogenase B [Salm...	23	628
gi 16766965 ref NP_462580.1	aldehyde dehydrogenase B [lact...	23	628
gi 27881830 gb AAH43675.1	similar to low density lipoprote...	23	628
gi 17088641 sp P98157 LRP1_CHICK	low-density lipoprotein rec...	23	628
gi 15599217 ref NP_252711.1	probable aldehyde dehydrogenas...	23	628
gi 32042075 ref NP_00139658.1	hypothetical protein [Pseudo...	23	628
gi 11684051 sp P37685 ALDB_ECOLI	Aldehyde dehydrogenase B (L...	23	628
gi 22985941 ref NP_00031048.1	hypothetical protein [Burkho...	23	628
gi 22986033 ref NP_00031138.1	hypothetical protein [Burkho...	23	628
gi 21240903 ref NP_640485.1	chloroacetaldehyde dehydrogena...	23	628
gi 23102047 ref NP_00088576.1	hypothetical protein [Azotob...	23	628

gi 2660722 gb AAC13641.1	chloroacetaldehyde dehydrogenase ...	23	628
gi 19836656 gb BAB1888.1	aldehyde dehydrogenase 1 [Actinet...	23	628
gi 15825096 gb AAL09567.1	lipoprotein receptor-related pro...	23	628
gi 17547847 ref NP_521249.1	PUTATIVE NAD+ DEPENDENT ACETAL...	23	628
gi 22963184 ref NP_00010790.1	hypothetical protein [Rhodop...	23	628
gi 22980082 ref NP_00025793.1	hypothetical protein [Ralsto...	23	628
gi 23867780 gb BAC21014.1	claudin4L2 [Xenopus laevis]	22	843
gi 18369662 emb CAD21635.1	putative dehydrogenase subunit ...	22	843
gi 12848262 gb BAB27889.1	unnamed protein product [Mus mu...	22	843
gi 25150357 ref NP_741619.1	Pro-collagen domains family me...	22	843
gi 15605825 ref NP_213202.1	hypothetical protein [Aquifex ...	22	843
gi 17093335 sp P21783 NOTC_XENLA	Neurogenic locus notch prot...	22	1131
gi 18859115 ref NP_571516.1	notch homolog 1a; neurogenic 1...	22	1131
gi 27675874 ref XP_228125.1	similar to 40kDa ribosomal pro...	22	1131
gi 1042521 P1F A35844	Xotch protein - African clawed frog	22	1131
gi 1293721 sp P10361 P53_RAT	Cellular tumor antigen p53 (Tum...	21	1518
gi 17259331 gb BAA92786.1	p53 (Macaca fuscata)	21	1518
gi 1894791 gb AA559989.1	p53 cellular tumor antigen	21	1518
gi 693787 gb BAB31269.1	tumour suppressor [Canis familiaris]	21	1518

Alignments

Get selected sequences

>gi 21355617 ref NP_651115.1	CG10873-PA [Drosophila melanogaster]
gi 17211767 gb AAF40427.1 AF224713_1	transcription factor p53 [Drosophila melano
gi 17211769 gb AAF40428.1 AF224714_1	transcription factor p53 [Drosophila melano
gi 17381624 gb AAF61572.1 AF244918_1	p53 tumor suppressor-like protein [Drosophi
gi 8272608 gb AAF74277.1 AF250918_1	transcription factor [Drosophila melanogast
gi 8453176 gb AAF75270.1 AF263722_1	transcription factor p53 [Drosophila melano
gi 10726710 gb AAF56087.2	CG10873-PA [Drosophila melanogaster]
gi 17861528 gb AAL39241.1	GH11591p [Drosophila melanogaster]
gi 18032162 gb AAL56639.1 AF192555_1	p53-like regulator of apoptosis and cell cyc

length = 385

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KVCPCPKRD 9  
K+CTCPCPKRD  
Sbjct: 259 KICPCPKRD 267

>gi|25009887|gb|AAN71112.1| AT28346p [Drosophila melanogaster]  
length = 519

Score = 31.6 bits (67), Expect = 1.3  
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KVCTCPKRD 9  
K+CTCPKRD  
Sbjct: 393 KICTCPKRD 401

>gi|31207283|ref|XP\_312608.1| ENSANGP0000014785 [Anopheles gambiae]  
gi|21295812|gb|EAA07957.1| ENSANGP0000014785 [Anopheles gambiae str. PEST]  
Length = 338

Score = 28.6 bits (60), Expect = 10  
Identities = 7/9 (77%), Positives = 9/9 (100%)

Query: 1 KVCTCPKRD 9  
K+C+CPKRD  
Sbjct: 309 KICSCPKRD 317

>gi|18150104|dbj|BAB83667.1| insulin receptor [Paralichthys olivaceus]  
Length = 1369

Score = 24.4 bits (50), Expect = 194  
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KVCTCPKRD 9  
KVC CPK D  
Sbjct: 705 KVCACPKTD 713

>gi|13626617|sp|O9TV36|FBN1\_PIG fibrillin 1 precursor  
gi|5739075|gb|AAD50328.1|AF073800.1 fibrillin-1 precursor [Sus scrofa]  
Length = 2871

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7  
VCTCPK  
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 100 CTCP 103

>gi|3688648|gb|AAC62317.1| mutant fibrillin-1 [Mus musculus]  
Length = 3857

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 2 VCTCPK 7  
VCTCPK  
Sbjct: 1775 VCTCPK 1780

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7  
VCTCPK  
Sbjct: 791 VCTCPK 796

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 100 CTCP 103

>gi|642072|gb|AAA61825.1| fibrillin-1  
Length = 1095

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7  
VCTCPK  
Sbjct: 766 VCTCPK 771

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 75 CTCP 78

>gi|13929178|ref|NP\_114013.1| fibrillin-1 [Rattus norvegicus]  
gi|4959650|gb|AAD34438.1| fibrillin-1 [Rattus norvegicus]  
Length = 2872

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7  
VCTCPK  
Sbjct: 790 VCTCPK 795

Score = 18.0 bits (35), Expect = 15950

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Sbjct: 100 CTCP 103

>gi|24430141|ref|NP\_000129.2| fibrillin 1 [Homo sapiens]  
Length = 2871

Score = 24.0 bits (49), Expect = 260

Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Sbjct: 100 CTCP 103

>gi|7459676|pir|AA7221 fibrillin 1 precursor - human (fragment)  
Length = 3002

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

Sbjct: 920 VCTCPK 925

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Sbjct: 231 CTCP 234

>gi|2494284|sp|Q61554|FBN1\_MOUSE fibrillin 1 precursor  
gi|1083318|pir|A55624 fibrillin-1 precursor - mouse  
gi|575510|gb|AA56840.1| fibrillin  
Length = 2871

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

VCTCPK  
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Sbjct: 100 CTCP 103

>gi|6679759|ref|NP\_032019.1| fibrillin 1; tight skin [Mus musculus]  
gi|726324|gb|AA64217.1| fibrillin-1  
Length = 2873

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

Sbjct: 791 VCTCPK 796

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Sbjct: 100 CTCP 103

>gi|27806637|ref|NP\_776478.1| fibrillin 1 [Bos taurus]  
gi|1706768|sp|P98133|FBN1\_BOVIN fibrillin 1 precursor (MP340)  
gi|1083029|pir|A55567 fibrillin I - bovine  
gi|508428|gb|AA74122.1| putative  
Length = 2871

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Sbjct: 100 CTCP 103

>gi|28487571|ref|XP\_192917.2| **L** fibrillin 1 [Mus musculus]  
Length = 2873

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7  
VCTCPK  
Sbjct: 791 VCTCPK 796

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 100 CTCP 103

>gi|544279|sp|P35555|FBN1\_HUMAN **L** Fibrillin 1 precursor  
gi|306746|gb|AA02036.1| **L** fibrillin  
gi|455958|gb|AB29419.1| fibrillin [human, Marfan syndrome patient, Peptide Mutan  
Length = 2871

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7  
VCTCPK  
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 100 CTCP 103

>gi|1335064|emb|CAA45118.1| **L** fibrillin [Homo sapiens]  
Length = 3002

Score = 24.0 bits (49), Expect = 260  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7  
VCTCPK  
Sbjct: 920 VCTCPK 925

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6  
CTCP  
Sbjct: 231 CTCP 234

>gi|729929|sp|P80424|LDI\_HIRME Leech-derived trypsin inhibitor (LDI)  
gi|7511702|pir|S50015 leech-derived trypsin inhibitor - medicinal leech  
gi|3212564|pdb|1DDT|L **S** Chain L, Complex Of Leech-Derived Trypsin Inhibitor With  
Porcine Trypsin

gi|3318723|pdb|1AN1|I **S** Chain I, Leech-Derived Trypsin Inhibitor (LDI)  
gi|998917|gb|AA33769.1| master cell trypsin inhibitor, LDI [Hirudo  
medicinalis=medical leeches, Peptide, 46 aa]  
Length = 46

Score = 23.5 bits (48), Expect = 349  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KVCACP 7  
KVC CPK  
Sbjct: 2 KVCACP 8

>gi|16506777|gb|AA23943.1|AF425233\_5 putative aldehyde dehydrogenase [Yersinia  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8  
VCTCPR R  
Sbjct: 300 VCTCPSR 306

>gi|21229579|ref|NP\_635496.1| chloroacetaldehyde dehydrogenase [Xanthomonas cam  
campestris str. ATCC 33913]  
gi|21111050|gb|AA039420.1| chloroacetaldehyde dehydrogenase [Xanthomonas campestr  
campestris str. ATCC 33913]  
Length = 509

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8  
VCTCPR R  
Sbjct: 303 VCTCPSR 309

>gi|17988030|ref|NP\_540664.1| ALDEHYDE DEHYDROGENASE [Brucella melitensis]  
gi|25284280|pir|AB3470 aldehyde dehydrogenase (NAD) (EC 1.2.1.3) [imported] - Br  
melitensis (strain 16M)  
gi|17983776|gb|AA152928.1| ALDEHYDE DEHYDROGENASE [Brucella melitensis 16M]  
Length = 505

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R  
Sbjct: 299 VCTCPSR 305

>gi|9652162|gb|AAF91420.1|AF277380.1 aldehyde dehydrogenase [Azotobacter vinelae]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R  
Sbjct: 300 VCTCPSR 306

>gi|23015854|ref|ZP\_00055619.1| hypothetical protein [Magnetospirillum magnetot-

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R  
Sbjct: 300 VCTCPSR 306

>gi|15597180|ref|NP\_250674.1| probable aldehyde dehydrogenase [Pseudomonas aeru-  
gi|11350931|pir|H83396 probable aldehyde dehydrogenase PA1984 [imported] - Pseud  
aeruginosa (strain PA01)  
gi|9947985|gb|AA05372.1|AE004625.2 probable aldehyde dehydrogenase [Pseudomonas  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R  
Sbjct: 300 VCTCPSR 306

>gi|28667956|ref|NP\_790575.1| aldehyde dehydrogenase family protein [Pseudomonas  
tomato str. DC3000]  
gi|28851192|gb|AA054270.1| aldehyde dehydrogenase family protein [Pseudomonas syr  
tomato str. DC3000]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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Sbjct: 300 VCTCPSR 306

>gi|23308979|ref|NP\_601988.2| NAD-dependent aldehyde dehydrogenase [Corynebacter  
ATCC 13032]  
gi|21325568|dbj|BAC00190.1| NAD-dependent aldehyde dehydrogenases [Corynebacteriu  
ATCC 13032]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R  
Sbjct: 301 VCTCPSR 307

>gi|23099989|ref|NP\_693455.1| aldehyde dehydrogenase [Oceanobacillus ihayensis f  
gi|22778220|dbj|BAC14490.1| aldehyde dehydrogenase [Oceanobacillus ihayensis HTE8  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R  
Sbjct: 300 VCTCPSR 306

>gi|15640836|ref|NP\_230467.1| aldehyde dehydrogenase [Vibrio cholerae]  
gi|11251887|pir|A82276 aldehyde dehydrogenase VC0819 [imported] - Vibrio cholera  
N16961 serogroup O1)  
gi|9655269|gb|AAF93982.1| aldehyde dehydrogenase [Vibrio cholerae]  
Length = 541

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R  
Sbjct: 335 VCTCPSR 341

>gi|2660726|gb|AAC13644.1| NAD-dependent chloroacetaldehyde dehydrogenase [Xanti  
autotrophicus]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VC TCP R  
Sbjct: 300 VCTCPSR 306

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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[>gi|23062066|ref|ZP\_00086869.1| hypothetical protein [Pseudomonas fluorescens Pf  
Length = 520

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 314 VCTCPSR 320

[>gi|15613244|ref|NP\_241547.1| aldehyde dehydrogenase [Bacillus halodurans]  
gi|25284184|pir|A83735 aldehyde dehydrogenase alda [imported] - Bacillus halodur  
(strain C-125)  
gi|10173295|dbj|BAB04400.1| aldehyde dehydrogenase [Bacillus halodurans]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 300 VCTCPSR 306

[>gi|15593281|gb|AAU02234.1|AF414083.5 putative truncated aldehyde dehydrogenase  
pseudotuberculosis]  
Length = 258

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 52 VCTCPSR 58

[>gi|30065134|ref|NP\_839305.1| aldehyde dehydrogenase B (lactaldehyde dehydrogen  
flexneri 2a str. 2457T)  
gi|30043395|gb|AAP1916.1| aldehyde dehydrogenase B (lactaldehyde dehydrogenase)  
flexneri 2a str. 2457T)  
Length = 542

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 336 VCTCPSR 342

[>gi|13475541|ref|NP\_107105.1| aldehyde dehydrogenase [Mesorhizobium loti]  
gi|14026293|dbj|BAB52891.1| aldehyde dehydrogenase [Mesorhizobium loti]

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Length = 505

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 299 VCTCPSR 305

[>gi|26989399|ref|NP\_744824.1| aldehyde dehydrogenase family protein [Pseudomonas  
gi|24984262|gb|AAN68288.1|AE016463.2 aldehyde dehydrogenase family protein [Pseud  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 300 VCTCPSR 306

[>gi|29833719|ref|NP\_828353.1| putative aldehyde dehydrogenase [Streptomyces averm  
gi|29610843|dbj|BAC74888.1| putative aldehyde dehydrogenase [Streptomyces avermit  
Length = 507

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 301 VCTCPSR 307

[>gi|17936107|ref|NP\_532897.1| aldehyde dehydrogenase [Agrobacterium tumefaciens  
Washington])  
gi|25284266|pir|AG2849 aldehyde dehydrogenase alda [imported] - Agrobacterium tu  
(strain C58, Dupont)  
gi|17740695|gb|AAU43213.1| aldehyde dehydrogenase [Agrobacterium tumefaciens str.  
Washington])  
Length = 505

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 299 VCTCPSR 305

[>gi|15283977|gb|AAK28545.2| putative aldehyde dehydrogenase [Yersinia pseudotub  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003



Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 300 VCTCPSR 306

>gi|15966104|ref|NP\_386457.1| PROBABLE ALDEHYDE DEHYDROGENASE PROTEIN [Sinorhizobium lotum]  
gi|15075374|emb|CAC46930.1| PROBABLE ALDEHYDE DEHYDROGENASE PROTEIN [Sinorhizobium lotum]  
Length = 502

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 296 VCTCPSR 302

>gi|27468985|ref|NP\_765622.1| glycine betaine aldehyde dehydrogenase gbsA [Staphylococcus epidermidis ATCC 12228]  
gi|27316534|gb|AA005709.1|AE016751.4 glycine betaine aldehyde dehydrogenase gbsA  
epidermidis ATCC 12228  
Length = 479

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 VCTCPKR 8  
VCTCP+R  
Sbjct: 285 VCTCPSR 291

>gi|15889500|ref|NP\_355181.1| AGR\_C\_4041p [Agrobacterium tumefaciens]  
gi|25284248|pir|E97626 chloroacetaldehyde dehydrogenase (AF029733) [imported] -  
Agrobacterium tumefaciens (strain C58, Cereon)  
gi|15157374|gb|AAK87966.1| AGR\_C\_4041p [Agrobacterium tumefaciens str. C58 (Cereon)]  
Length = 540

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 334 VCTCPSR 340

>gi|24375958|ref|NP\_720001.1| aldehyde dehydrogenase [Shewanella oneidensis MR-1]  
gi|24350948|gb|AA57445.1|AE015880.4 aldehyde dehydrogenase [Shewanella oneidensis MR-1]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R

Sbjct: 300 VCTCPSR 306

>gi|24114856|ref|NP\_709366.1| aldehyde dehydrogenase B (lactaldehyde dehydrogenase B) [Flexneri 2a str. 301]  
gi|24054091|gb|AA45073.1|AE015370.10 aldehyde dehydrogenase B (lactaldehyde dehydrogenase B) [Flexneri 2a str. 301]  
Length = 558

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 352 VCTCPSR 358

>gi|16152093|gb|AA14969.1|AF418982.6 putative aldehyde dehydrogenase [Yersinia enterocolitica]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 300 VCTCPSR 306

>gi|3928680|gb|AAC79659.1| NAD+ dependent acetaldehyde dehydrogenase [Pseudomonas aeruginosa]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 300 VCTCPSR 306

>gi|1519175|dbj|BAA75508.1| aldehyde dehydrogenase [petroleum-degrading bacterium]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 300 VCTCPSR 306

>gi|27379895|ref|NP\_771424.1| aldehyde dehydrogenase [Bradyrhizobium japonicum]  
gi|27353048|dbj|BAC50049.1| aldehyde dehydrogenase [Bradyrhizobium japonicum USDA]  
Length = 505

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 299 VCTCPSR 305

>gi|23469955|ref|ZP\_00125289.1| hypothetical protein [Pseudomonas syringae pv. ]  
Length = 506

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 300 VCTCPSR 306

>gi|21219685|ref|NP\_625464.1| aldehyde dehydrogenase [Streptomyces coelicolor A:  
gi|8928070|sp|Q9R3Z6|DHAL\_STRCO Probable aldehyde dehydrogenase  
gi|6468426|emb|CAB61586.1| aldehyde dehydrogenase [Streptomyces coelicolor A3(2)]  
Length = 507

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 301 VCTCPSR 307

>gi|15825005|gb|AL09566.1|AF367720.1 [ lipoprotein receptor-related protein (M  
Length = 4545

Score = 22.7 bits (46), Expect = 628  
Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 2/9 (22%)

Query: 2 VCTCP--KR 8  
VCTCP KR  
Sbjct: 4169 VCTCPNGKR 4177

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCTCP 6  
VC+CP  
Sbjct: 1206 VCSCP 1210

>gi|23008217|ref|ZP\_00049754.1| hypothetical protein [Magnetospirillum magnetot:  
Length = 260

Score = 22.7 bits (46), Expect = 628  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8  
VCTCP R  
Sbjct: 54 VCTCPSR 60

Get selected sequences Select all Deselect all

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
Posted date: Jul 10, 2003 1:49 AM  
Number of letters in database: 474,244,320  
Number of sequences in database: 1,477,204

Lambda K H  
0.360 0.295 2.12

Gapped  
Lambda K H  
0.294 0.110 0.610

Matrix: PAM30  
Gap Penalties: Existence: 9, Extension: 1  
Number of Hits to DB: 7,726,919  
Number of Sequences: 1477204  
Number of extensions: 34981  
Number of successful extensions: 1887  
Number of sequences better than 20000.0: 100  
Number of HSP's better than 20000.0 without gapping: 1713  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1887  
length of query: 9  
length of database: 474,244,320  
effective HSP length: 0  
effective length of query: 9  
effective length of database: 474,244,320  
effective search space: 4268198880  
effective search space used: 4268198880  
T: 11  
A: 40  
X1: 14 (7.3 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 35 (19.9 bits)  
S2: 35 (18.0 bits)

EXHIBIT M

RID=1057871489-08294-14294, SEQID31

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# NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

## Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057871489-08294-14294

Query= SEQID31  
(7 letters)

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

## Distribution of 90 Blast Hits on the Query Sequence

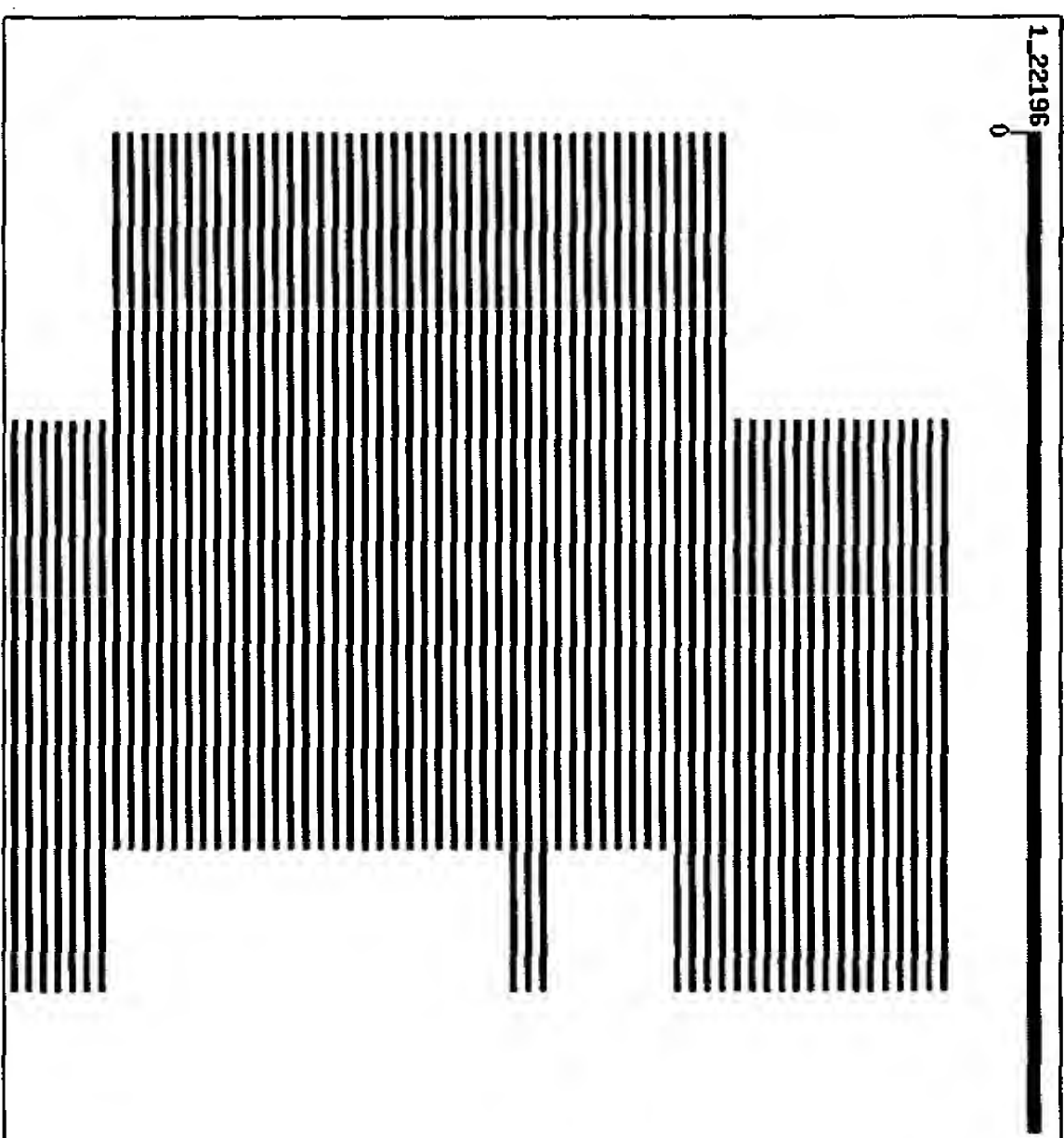
Mouse-over to show define and scores. Click to show alignments

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

RID=1057871489-08294-14294, SEQID31

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Sequences producing significant alignments:

	Score (bits)	E value
gi 17981441 gb AA151006.1 AF454393.1 folliculin [Drosophil...	21	2733
gi 23822094 sp Q8SPZ8 RMS8_PANTR ribonuclease 8 precursor (...)	21	2733
gi 17508299 ref NP_490910.1 Predicted CDS, f-box domain co...	21	2733
gi 23613363 ref NP_703207.1 erythrocyte membrane protein 1...	21	2733
gi 22024157 ref NP_611024.2 CG12956-PA [Drosophila melanog...	21	2733
gi 22988530 ref ZP_00033594.1 hypothetical protein [Burkho...	21	2733
gi 6537223 gb AA15567.1 AF179376.2 Orf2 [Mycoplasma ferme...	21	2733
gi 28317234 gb AA039624.1 GH04473p [Drosophila melanogaster]	21	2733
gi 31072003 tpq DAA01353.1 TPA: DEFB106-like protein [Pap...	21	2733
gi 9629715 ref NP_045007.1 putative viral coat protein dup...	21	2733
gi 9625926 ref NP_040174.1 DNA helicase-primase complex [H...	21	2733
gi 7385025 gb AA61653.1 AF206304.4 ORF52 [Human herpesvitu...	21	2733
gi 31196303 ref XP_307099.1 ENSNANP0000022845 [Anopheles ...]	21	2733
gi 21687143 ref NP_612204.1 RNase 8, placental [Homo sapie...	21	2733
gi 15088547 gb AAK84083.1 AF326781.9 putative resistance pr...	21	2733
gi 666132 gb AA62240.1 transcriptional activator	19	8859
gi 10176803 dbj BA009991.1 mutator-like transposase-like [...]	19	8859
gi 32404470 ref XP_322848.1 predicted protein [Neurospora ...]	19	8859
gi 21362028 ref NP_078933.2 hypothetical protein FLJ11565 ...	19	8859

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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gi 18253297 gb AA166410.1	NPY receptor [Lampetra fluviatilis]	19	8859	
gi 17555566 ref NP_497427.1	Putative nuclear protein, with...	19	8859	<b>E</b>
gi 21492735 ref NP_659810.1	unknown [Rhizobium etli] >gi 1...	19	8859	
gi 20804175 emb CAD31378.1	PROBABLY NIF-SPECIFIC REGULATOR...	19	8859	
gi 20892831 ref XP_153922.1	hypothetical protein XP_153922...	19	8859	<b>E</b>
gi 116902 sp P1149 COL_SQUAC	Colipase >gi 85421 pir  A0533...	19	8859	
gi 18643741 emb CAD23056.1	du75H8.2 (similar to KIAA0136 p...	19	8859	
gi 15668931 ref NP_247735.1	ferredoxin-type protein (naph)...	19	8859	
gi 28528164 ref XP_135851.2	RIKEN cDNA B930011H20 gene [Mu...	18	11887	<b>E</b>
gi 9625894 ref NP_040142.1	ribonucleotide reductase, large...	18	11887	
gi 13242411 ref NP_077434.1	ribonucleotide reductase, larg...	18	11887	
gi 30147766 ref XP_301761.1	similar to peptidyl-Pro cis tr...	18	11887	<b>E</b>
gi 24650321 ref NP_651480.1	CG14238-PA [Drosophila melanog...	18	11887	<b>E</b>
gi 15238307 ref NP_199032.1	family II lipase EXL3, putativ...	18	11887	
gi 20090513 ref NP_616588.1	hypothetical protein (multi-do...	18	15950	
gi 29733668 ref XP_291251.1	similar to ADAM 7 precursor (A...	18	15950	<b>E</b>
gi 485335 gb AA25025.1	ureg	18	15950	
gi 27703880 ref XP_230727.1	similar to defensin, beta 129;...	18	15950	<b>E</b>
gi 31239543 ref XP_320185.1	ENSANGP0000011153 [Anopheles ...	18	15950	
gi 26352394 dbj BAC39827.1	unnamed protein product [Mus mu...	18	15950	<b>E</b>
gi 32480006 emb CAE01650.1	OSJNB0021110.14 [Oryza sativa ...	18	15950	
gi 6321991 ref NP_012067.1	Involved in Processing ITS2; Yh...	18	15950	
gi 13959319 sp Q61129 CFAI_MOUSE	Complement factor I precur...	18	15950	<b>E</b>
gi 17461179 ref XP_066597.1	similar to tyrosine 3/tryptoph...	18	15950	<b>E</b>
gi 1561134 ref NP_222785.1	UREASE ACCESSORY PROTEIN [Hel1...	18	15950	
gi 31243045 ref XP_321957.1	ENSANGP0000013922 [Anopheles ...	18	15950	
gi 1314734 gb AA09804.1	220 kDa silk protein	18	15950	
gi 730843 sp P40798 STC_DROME	Shuttle craft protein >gi 751...	18	15950	<b>E</b>
gi 31207579 ref XP_312756.1	ENSANGP0000003142 [Anopheles ...	18	15950	
gi 20137329 sp Q28475 AD07_MACPA	ADAM 7 precursor (A disint...	18	15950	
gi 16758958 ref NP_446081.1	folliclestatin-like 3 [Rattus nor...	18	15950	<b>E</b>
gi 5031701 ref NP_005851.1	folliclestatin-like 3 glycoprotei...	18	15950	<b>E</b>
gi 20901710 ref XP_156971.1	hypothetical protein XP_156971...	18	15950	<b>E</b>
gi 6324605 ref NP_014674.1	Metallothionein-like protein; C...	18	15950	
gi 23021838 ref ZP_00061491.1	hypothetical protein [Clostr...	18	15950	
gi 13878203 ref NP_113557.1	folliclestatin-like 3; E030038F23...	18	15950	<b>E</b>
gi 27731549 ref XP_218624.1	similar to adaptor-related pro...	18	15950	<b>E</b>
gi 3643253 gb AAC36742.1	sperm maturation-related glycopro...	18	15950	<b>E</b>
gi 20137479 sp Q9H2U9 AD07_HUMAN	ADAM 7 precursor (A disint...	18	15950	<b>E</b>
gi 15899907 ref NP_344512.1	Conserved hypothetical protein...	18	15950	
gi 13162353 ref NP_077071.1	complement factor I [Rattus no...	18	15950	<b>E</b>
gi 28511186 ref XP_289852.1	similar to H-2 class I histoco...	18	15950	<b>E</b>
gi 2739186 gb AA094621.1	glycoprotein A [Pneumocystis cari...	18	15950	
gi 15644698 ref NP_206868.1	urease accessory protein (ureg...	18	15950	
gi 32398676 emb CAD98636.1	similar to glycogen debranching...	18	15950	
gi 24651113 ref NP_651716.1	CG1964-PA [Drosophila melanoga...	18	15950	<b>E</b>
gi 27718485 ref XP_235189.1	similar to 60S RIBOSOMAL PROTE...	18	15950	<b>E</b>
gi 6671561 ref NP_031484.1	adaptor protein complex AP-2, a...	18	15950	<b>E</b>
gi 15237177 ref NP_197688.1	expressed protein (Arabidopsis...	18	15950	
gi 19309738 emb CAD24841.1	laccase [Gaeumannomyces graminii...	18	15950	
gi 28175506 gb AA043207.1	Unknown (protein for IMAGE:52950...	18	15950	
gi 27497797 gb AA013155.1	substrate adhesion molecule prec...	18	15950	

gi 5913966 dbj BA084537.1	urease G [Helicobacter pylori]	18	15950	
gi 4926957 gb AA032965.1	complement factor I [Mus musculus]	18	15950	<b>E</b>
gi 416704 sp Q03376 BAR3_CHITRE	Balbiani RING protein 3 prec...	18	15950	
gi 22946527 gb AA010891.1	CG3647-PA [Drosophila melanogaster]	18	15950	<b>E</b>
gi 11359837 pir T44598	hypothetical protein (imported) - f...	18	15950	<b>E</b>
gi 31202639 ref XP_310268.1	ENSANGP0000015231 [Anopheles ...	18	15950	
gi 24213057 ref NP_710538.1	conserved hypothetical protein...	18	15950	
gi 31195615 ref XP_306755.1	ENSANGP0000013672 [Anopheles ...	18	15950	
gi 3126641 dbj BA026002.1	similar to adenyl cyclase asso...	18	15950	
gi 22164216 gb AA093613.1	AP483691.1 putative secreted prot...	18	15950	
gi 22164198 gb AA093604.1	AF483682.1 putative secreted prot...	18	15950	
gi 19171194 emb CAD10747.1	laccase [Gaeumannomyces graminii...	18	15950	
gi 6671744 ref NP_031712.1	complement component factor i [...	18	15950	<b>E</b>
gi 19343434 ref NP_597914.1	polymerase [Northern cereal mo...	18	15950	

## Alignments

Get selected sequences	Select all	Deselect all
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>gi|17981441|gb|AA151006.1|AF454393.1 folliclestatin [Drosophila melanogaster]  
Length = 705

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 542 CKNSC 546

>gi|23822094|sp|Q8SP28|RNS8\_PANTR Ribonuclease 8 precursor (RNase 8)  
gi|19525682|gb|AA189645.1|AF473855.1 RNase 8 [Pan troglodytes]  
Length = 157

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 92 CKNSC 96

>gi|17508299|ref|NP\_490910.1| **E** Predicted CDS, f-box domain containing protein 1  
[Caenorhabditis elegans]  
gi|7505868|pir|T15284 hypothetical protein M01D7.1 - Caenorhabditis elegans  
gi|2105486|gb|AA58068.1| Hypothetical protein M01D7.1 [Caenorhabditis elegans]  
Length = 339

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7

CKNSC  
Sbjct: 46 CKNSC 50

>gi|23613363|ref|NP\_703207.1| erythrocyte membrane protein 1 (PfEMP1) [Plasmodi  
gi|7670005|emb|CAB8209.1| erythrocyte membrane protein 1 (PfEMP1) [Plasmodium fa  
length = 2163

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 633 CKNSC 637

>gi|22024157|ref|NP\_611024.2| CG12956-PA [Drosophila melanogaster]  
gi|21627146|gb|AAF58157.2| CG12956-PA [Drosophila melanogaster]  
length = 581

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 475 CKNSC 479

>gi|22988530|ref|NP\_00033594.1| hypothetical protein [Burkholderia fungorum]  
length = 416

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 58 CKNSC 62

>gi|6537223|gb|AAF15567.1|AF179376.2 OrfE2 [Mycoplasma fermentans]  
length = 48

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 28 CKNSC 32

>gi|28317234|gb|AAO39624.1| GH04473p [Drosophila melanogaster]  
length = 767

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 604 CKNSC 608

>gi|31072003|tpg|DAA01353.1| TPA: DEFBI06-like protein [Papio anubis]  
length = 57

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 33 CKNSC 37

>gi|9629715|ref|NP\_045007.1| putative viral coat protein duplicate (CPd) [Little  
gi|1620423|emb|CAA63729.1| ORF4, putative viral coat protein duplicate gene [Little  
virus 1]  
gi|2398674|emb|CAA71290.1| putative viral coat protein duplicate (CPd) [Little ch  
length = 664

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 286 CKNSC 290

>gi|9625926|ref|NP\_040174.1| DNA helicase-primase complex [Human herpesvirus 3]  
gi|136804|sp|P09300|HEPA\_VZVD DNA HELICASE/PRIMASE COMPLEX ASSOCIATED PROTEIN  
gi|73884|pir|WZBE52 gene 52 protein - human herpesvirus 3  
gi|60041|emb|CAA27935.1| ORF 52 (AA1-771) [Human herpesvirus 3]  
length = 771

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 43 CKNSC 47

>gi|7385025|gb|AAF61653.1|AF206304.4 ORF52 [Human herpesvirus 3]  
length = 771

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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Sbjct: 43 CKNSC 47

>gi|31196303|ref|XP\_307099.1| ENSANGP0000022845 [Anopheles gambiae]  
gi|30179369|gb|EAA45752.1| ENSANGP0000022845 [Anopheles gambiae str. PEST]  
Length = 182

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 141 CKNSC 145

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 81 CKNSC 85

>gi|21687143|ref|NP\_612204.1| RNase 8, placental [Homo sapiens]  
gi|23822095|sp|O8TDE3|RNS8\_HUMAN Ribonuclease 8 precursor (RNase 8)  
gi|19525680|gb|AA189644.1|AF473854.1 RNase 8 [Homo sapiens]  
Length = 154

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 89 CKNSC 93

>gi|15088547|gb|AAK84083.1|AF326781.9 putative resistance protein [Triticum mon  
Length = 907

Score = 20.6 bits (41), Expect = 2733  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CKNSC  
Sbjct: 278 CKNSC 282

>gi|666132|gb|AA62240.1| transcriptional activator  
Length = 584

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 469 FACKNS 474

>gi|10176803|dbj|BAB09991.1| mutator-like transposase-like [Arabidopsis thaliana]  
Length = 825

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 1 FXCKNSC 7  
F CK+SC  
Sbjct: 548 FGCKSSC 554

>gi|32404470|ref|XP\_322848.1| predicted protein [Neurospora crassa]  
gi|28919646|gb|EAA29063.1| predicted protein [Neurospora crassa]  
Length = 705

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCKNSC 7  
F CK SC  
Sbjct: 386 FACKTSC 392

>gi|21362028|ref|NP\_078933.2| hypothetical protein FLJ11565 [Homo sapiens]  
gi|16551580|dbj|BAB71125.1| unnamed protein product [Homo sapiens]  
Length = 760

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 145 FSCKNS 150

>gi|18253297|gb|ALU66410.1| NPY receptor [Lampetra fluviatilis]  
Length = 365

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 358 FSCKNS 363

>gi|17555566|ref|NP\_497427.1| Putative nuclear protein, with a coiled coil-4 c  
specific [Caenorhabditis elegans]



gi|15145438|gb|AAK84598.1|AC084153.16 Hypothetical protein Y22D7AL.9 [Caenorhabditis elegans]  
Length = 668

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 435 FSCCKNS 440

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 323 FSCCKNS 328

gi|21492735|ref|NP\_659810.1| unknown [Rhizobium etli]  
gi|1709273|sp|P54931|NIFA\_RHIEF Nif-specific regulatory protein  
gi|1144325|gb|AA84917.1| NifA  
gi|21467160|gb|AA54823.1| unknown [Rhizobium etli]  
Length = 584

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 469 FACKNS 474

gi|20804175|emb|CAD31378.1| PROBABLE NIF-SPECIFIC REGULATORY PROTEIN ACTIVATOR  
DNA-BINDING NIFA [Mesorhizobium loti]  
Length = 586

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 469 FACKNS 474

gi|20892831|ref|XP\_153922.1| hypothetical protein XP\_153922 [Mus musculus]  
Length = 115

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 104 FSCCKNS 109

gi|116902|sp|P11149|COL\_SQUAC Colipase  
gi|854221|pir|A05331 colipase - spiny dogfish (fragment)  
Length = 39

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 1 FXCKNSC 7  
F CK+SC  
Sbjct: 20 PQCKSSC 26

gi|18643741|emb|CAD23056.1| dJ75H8.2 (similar to KIAA0136 protein) [Homo sapiens]  
Length = 903

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 288 FSCCKNS 293

gi|15668931|ref|NP\_247735.1| ferredoxin-type protein (napH) [Methanococcus jannaschii]  
gi|2128473|pir|F64393 hypothetical protein MJ0750 - Methanococcus jannaschii  
gi|1592304|gb|AA898746.1| ferredoxin-type protein (napH) [Methanococcus jannaschii]  
Length = 238

Score = 18.9 bits (37), Expect = 8859  
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 1 FXCKNSC 7  
F CK+SC  
Sbjct: 217 FECKSSC 223

gi|28528164|ref|XP\_135851.2| RIKEN CDNA B930011H20 gene [Mus musculus]  
gi|31542182|ref|NP\_848897.2| RIKEN CDNA B930011H20 gene [Mus musculus]  
gi|26348945|dbj|BAC38112.1| unnamed protein product [Mus musculus]  
Length = 1358

Score = 18.5 bits (36), Expect = 11887  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 671 FTCKNS 676

gi|9625894|ref|NP\_040142.1| ribonucleotide reductase, large subunit [Human hery  
gi|132612|sp|P09248|RI11\_VZVD RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (R  
REDUCTASE)



gi|66405|pic|WMBE19 ribonucleoside-diphosphate reductase (EC 1.17.4.1) large cha  
human herpesvirus 3  
gi|60008|emb|CAA27902.1| ORF19 (AA1-775) [Human herpesvirus 3]  
Length = 775

Score = 18.5 bits (36), Expect = 11887  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCKNSC 7  
F CK SC  
Sbjct: 487 FPCKKSC 493

gi|13242411|ref|NP\_077434.1| ribonucleotide reductase, large subunit [Cercopit  
71  
gi|11036563|gb|AAG27192.1|AF275348\_12 ribonucleotide reductase, large subunit [Ce  
71  
Length = 783

Score = 18.5 bits (36), Expect = 11887  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCKNSC 7  
F CK SC  
Sbjct: 495 FPCKKSC 501

gi|30147766|ref|XP\_301761.1| similar to peptidyl-Pro cis trans isomerase [Hon  
Length = 208

Score = 18.5 bits (36), Expect = 11887  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCKNSC 7  
F CK SC  
Sbjct: 119 PACKASC 125

gi|24650321|ref|NP\_651480.1| CG14238-PA [Drosophila melanogaster]  
gi|7301471|gb|AAF56595.1| CG14238-PA [Drosophila melanogaster]  
Length = 523

Score = 18.5 bits (36), Expect = 11887  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 296 FTCKNS 301

gi|15238307|ref|NP\_199032.1| family II lipase EXL3, putative [Arabidopsis thal;  
gi|9757962|db|BAB08450.1| GDSL-motif lipase/hydrolase-like protein [Arabidopsis  
Length = 319

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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Score = 18.5 bits (36), Expect = 11887  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 282 FTCKNS 287

gi|20090513|ref|NP\_616588.1| hypothetical protein (multi-domain) [Methanosarci  
str. C2A]  
gi|19915538|gb|AAM05068.1| hypothetical protein (multi-domain) [Methanosarcina ac  
str. C2A]  
Length = 955

Score = 18.0 bits (35), Expect = 15950  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 361 FTCKNS 366

gi|29733668|ref|XP\_291251.1| similar to ADAM 7 precursor (A disintegrin and r  
domain 7) (Sperm maturation-related glycoprotein GP-83)  
[Homo sapiens]  
Length = 754

Score = 18.0 bits (35), Expect = 15950  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 490 FPCKNS 495

gi|485335|gb|AAA25025.1| ureg  
Length = 199

Score = 18.0 bits (35), Expect = 15950  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 46 FMCKNS 51

gi|27703880|ref|XP\_230727.1| similar to defensin, beta 129, defensin, beta 2;  
open reading frame 87 [Homo sapiens] [Rattus  
norvegicus]  
Length = 164

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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CK+SC  
Sbjct: 34 CKDSC 38

>gi|31239543|ref|XP\_320185.1| ENSANGP00000011153 [Anopheles gambiae]  
gi|30174007|gb|EAA00393.2| ENSANGP00000011153 [Anopheles gambiae str. PEST]  
Length = 4569

Score = 18.0 bits (35), Expect = 15950  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 1014 FECKNS 1019

>gi|26352394|dbj|BAC39827.1| unnamed protein product [Mus musculus]  
Length = 257

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 93 CKDSC 97

>gi|32480006|emb|CAE01650.1| OSJNB0021110.14 [Oryza sativa (japonica cultivar-gi|32480127|emb|CAE01940.1| OSJNB0073L13.2 [Oryza sativa (japonica cultivar-grou  
Length = 459

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 306 CKDSC 310

>gi|6321991|ref|NP\_012067.1| Involved in Processing ITS2; Yhr197wp [Saccharomyc  
gi|731766|sp|P38883|YHZ7\_YEAST HYPOTHETICAL 86.7 KD PROTEIN IN EGD2-SUN1 INTERGEN  
gi|626699|pir|S46678| hypothetical protein YHR197w - yeast (Saccharomyces cerevis  
gi|458930|gb|AAB68356.1| Yhr197wp [Saccharomyces cerevisiae]  
Length = 763

Score = 18.0 bits (35), Expect = 15950  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 514 FVCKNS 519

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|13959319|sp|Q61129|CPAI\_MOUSE Complement factor I precursor (C3B/C4B inact  
Length = 603

Score = 18.0 bits (35), Expect = 15950  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 142 FICCKNS 147

>gi|17461179|ref|XP\_066597.1| similar to tyrosine 3/tryptophan 5 -monooxygenas  
protein, zeta polypeptide; protein kinase C inhibitor  
protein-1; phospholipase A2; 14-3-3 zeta [Homo sapiens]  
Length = 118

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 113 CKDSC 117

>gi|15611134|ref|NP\_222785.1| UREASE ACCESSORY PROTEIN [Helicobacter pylori J99;  
gi|7388360|sp|Q9ZM27|UREG\_HELPJ Urease accessory protein ureg  
gi|7447466|pir|C71979| urease accessory protein ureg [similarity] - Helicobacter  
(strain J99)  
gi|4154571|gb|AAD05647.1| UREASE ACCESSORY PROTEIN [Helicobacter pylori J99]  
Length = 199

Score = 18.0 bits (35), Expect = 15950  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 46 FMCKNS 51

>gi|31243045|ref|XP\_321957.1| ENSANGP00000013922 [Anopheles gambiae]  
gi|21289514|gb|EAA01807.1| ENSANGP00000013922 [Anopheles gambiae str. PEST]  
Length = 1557

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 1529 CKDSC 1533

>gi|1314734|gb|AAA99804.1| 220 kDa silk protein  
Length = 1704

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 312 CKDSC 316

[>gi|730843|sp|P40798|STC\_DROME Shuttle craft protein  
gi|7511869|pir|T13938 gene shuttle craft protein - fruit fly (Drosophila melanog  
gi|487400|gb|AAB60255.1| shuttle craft protein [Drosophila melanogaster]  
Length = 1106

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 590 CKDSC 594

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 575 CKDSC 579

[>gi|31207579|ref|XP\_312756.1| ENSANGP00000003142 [Anopheles gambiae]  
gi|30177153|gb|EAA08447.2| ENSANGP00000003142 [Anopheles gambiae str. PE8T]  
Length = 1204

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 678 CKDSC 682

[>gi|20137329|sp|Q28475|AD07\_MACFA ADAM 7 precursor (A disintegrin and metallopro  
(Epididymal apical protein I) (EAP I)  
gi|283937|pir|S28258 androgen-regulated epididymal protein precursor - crab-eati  
macaque  
gi|38063|emb|CAA46929.1| epididymal apical protein I-precursor [Macaca fascicular  
Length = 776

Score = 18.0 bits (35), Expect = 15950  
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Query: 1 FXCKNS 6  
F CKNS  
Sbjct: 490 FXCKNS 495

[>gi|16758958|ref|NP\_446081.1| follistatin-like 3 [Rattus norvegicus]  
gi|23821549|sp|Q99PW7|FSL3\_RAT Follistatin-related protein 3 precursor (Follistat  
(Follistatin-related gene protein)  
gi|12964594|dbj|BAB32664.1| follistatin-related protein FLRG [Rattus norvegicus  
gi|23095929|dbj|BAC16229.1| follistatin-like protein [Rattus norvegicus]  
Length = 256

Score = 18.0 bits (35), Expect = 15950  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7  
CK+SC  
Sbjct: 93 CKDSC 97

Get selected sequences

Select all

Deselect all

Database: All non-redundant Genbank CDS  
translations+PDB+SwissProt+PIR+PIR  
Posted date: Jul 10, 2003 1:49 AM  
Number of letters in database: 474,244,320  
Number of sequences in database: 1,477,204

Lambda K H  
0.366 0.280 2.29

Gapped  
Lambda K H  
0.294 0.110 0.610

Matrix: PAM30  
Gap Penalties: Existence: 9, Extension: 1  
Number of Hits to DB: 3,751,296  
Number of Sequences: 1477204  
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Number of HSP's better than 20000.0 without gapping: 85  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 90  
Length of query: 7  
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Effective HSP length: 0  
Effective length of query: 9  
Effective length of database: 474,244,320  
Effective search space: 4268198880  
Effective search space used: 4268198880  
T: 11  
A: 40  
X1: 14 ( 7.4 bits)  
X2: 35 (14.8 bits)

X3: 58 (24.6 bits)  
S1: 35 (20.3 bits)  
S2: 35 (18.0 bits)

## REPORTS

igin for the loris-lemur clade cannot be ruled out (24) in the light of this new discovery. A similar scenario (adapted from molecular data) has been suggested for endemic Malagasy rodents (32).

The possibility that lemuriforms and lorisiforms originated in Asia rather than in Africa cannot be rejected without further paleontological evidence from both continents and from Madagascar. It must, however, be emphasized that their origin is undoubtedly as ancient as that of adapiforms (Fig. 3A). The discovery of a cheirogaleid-like lemur in Oligocene deposits of Pakistan suggests that whatever the timing and direction of faunal dispersions, South Asia was, as for anthropoids (33), an important theater of early strepsirrhine evolution, reflecting the complex role played by the drifting Greater India in the evolutionary history of Malagasy lemurs.

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36. We are indebted to Nawab Mohammad Akbar Khan Bugti, Lord of the Bugti Tribes, and to Shahid Hassan Bugti for their total fieldwork assistance, to I. Akhund for his help, and to Bahadur Khan Rodani, Vice Chancellor of the University of Balochistan. We thank R. D. Martin for providing us useful comments on the manuscript. Many thanks to C. Denys and J. Cuisin (MNHN, Paris) for access to comparative material and to B. Marandat for preparing fossils. This work was funded by the University of Montpellier (CNRS-UMR 5554), the MNHN, Paris (CNRS-UMR 8569), the Fyssen, Leakey, Wenner-Gren, Singer-Polignac, Bleustein-Blanchet and Treilles Foundations. This is ISEM publication 2001-107.

9 August 2001; accepted 12 September 2001

## Caenorhabditis elegans p53: Role in Apoptosis, Meiosis, and Stress Resistance

W. Brent Derry,\* Aaron P. Putzke, Joel H. Rothman

We have identified a homolog of the mammalian p53 tumor suppressor protein in the nematode *Caenorhabditis elegans* that is expressed ubiquitously in embryos. The gene encoding this protein, *cep-1*, promotes DNA damage-induced apoptosis and is required for normal meiotic chromosome segregation in the germ line. Moreover, although somatic apoptosis is unaffected, *cep-1* mutants show hypersensitivity to hypoxia-induced lethality and decreased longevity in response to starvation-induced stress. Overexpression of CEP-1 promotes widespread caspase-independent cell death, demonstrating the critical importance of regulating p53 function at appropriate levels. These findings show that *C. elegans* p53 mediates multiple stress responses in the soma, and mediates apoptosis and meiotic chromosome segregation in the germ line.

The p53 tumor suppressor is among the most frequently mutated genes in human cancer and plays a critical role in maintaining genomic stability by regulating cell cycle progression and apoptosis in response to DNA damage (1, 2). Analysis of the mechanisms through which p53 integrates the cellular response to stress and damage in vivo has been limited by the absence of a genetic system. Recently, a p53 homolog was shown to participate in apoptosis induced by genotoxic stress in *Drosophila* (3–5) on the basis of forced expression of dominant negative forms; however, the organism-wide role of the gene could not be assessed in these experiments.

Standard searches of the genomic sequence suggested that *C. elegans* does not have a p53-like gene (6). However, using additional algorithms, we identified a *C. elegans* gene encoding a protein with signature sequences common to the p53 family, includ-

ing the residues most frequently mutated in human cancers (7). The cDNA sequence of this gene, *cep-1* (denoting *C. elegans* p53-like-1), predicts a 429-amino acid protein that is similar to the human protein in the NH<sub>2</sub>-terminal transactivation domain and the highly conserved DNA binding domains (Fig. 1). CEP-1 appears to be the only p53 family member encoded in the *C. elegans* genome, which suggests that p53 paralogs (including p63 and p73) may have evolved from a single ancestor related to CEP-1.

To assess the in vivo function of *cep-1*, we isolated a chromosomal rearrangement, *cep-1(w40)* (8). This mutant strain contains an intact copy of *cep-1* at its normal genomic location; the *cep-1(w40)* mutant gene, which encodes a truncated protein lacking the DNA binding domain, is translocated elsewhere in the genome. Although they exhibit impenetrant (~2%) embryonic lethality, *cep-1(w40)* mutants are generally viable and fertile. Moreover, depleting *cep-1* function by RNA interference (RNAi) (9) similarly leads to impenetrant embryonic lethality (Table 1). It is likely that RNAi results in a strong loss-of-function phenotype, as it eliminates detectable expression of a CEP-1::GFP

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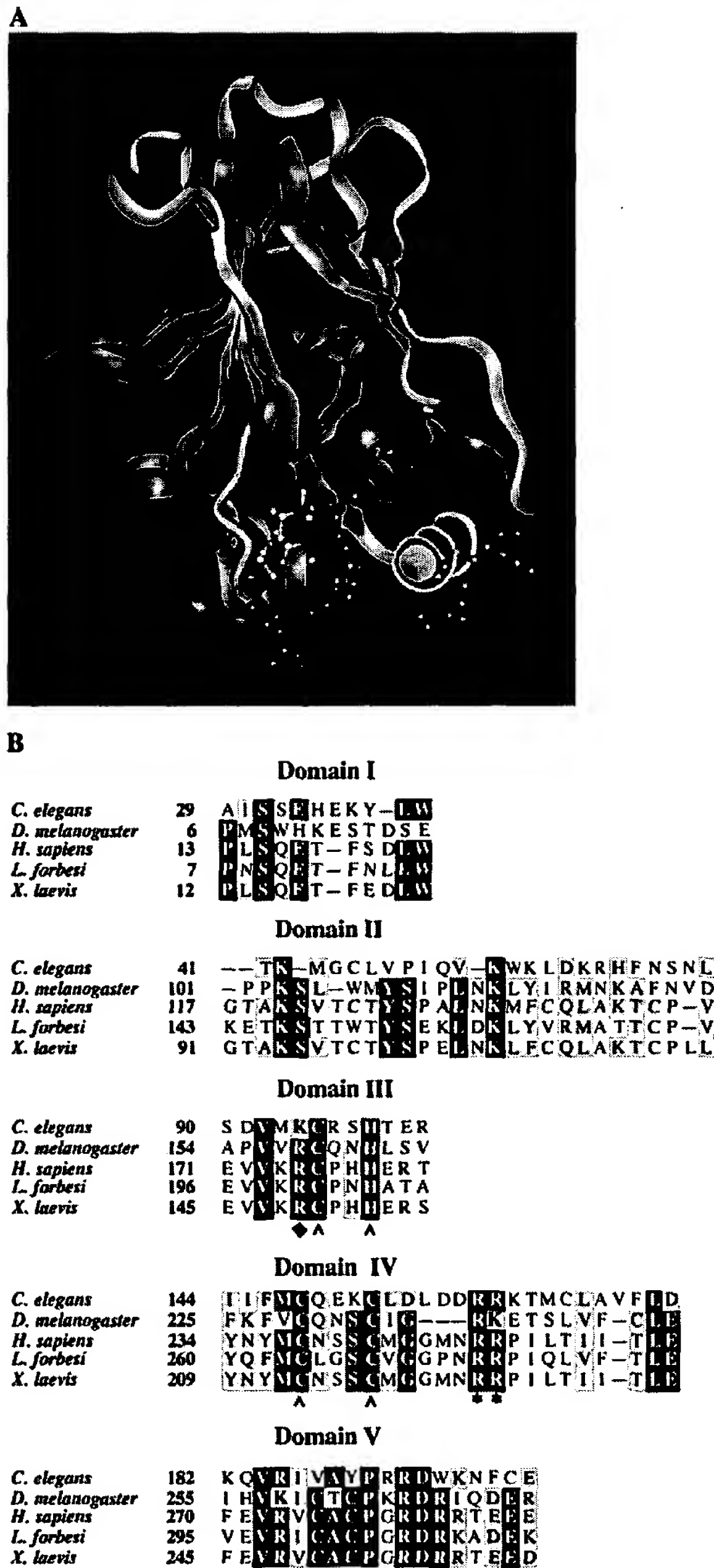
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(green fluorescent protein) reporter (10). We found that both *cep-1(w40)* and *cep-1(RNAi)* embryos undergo a normal pattern of somatic apoptosis, suggesting that CEP-1 is not re-

quired for developmental programmed cell death in the soma (10).

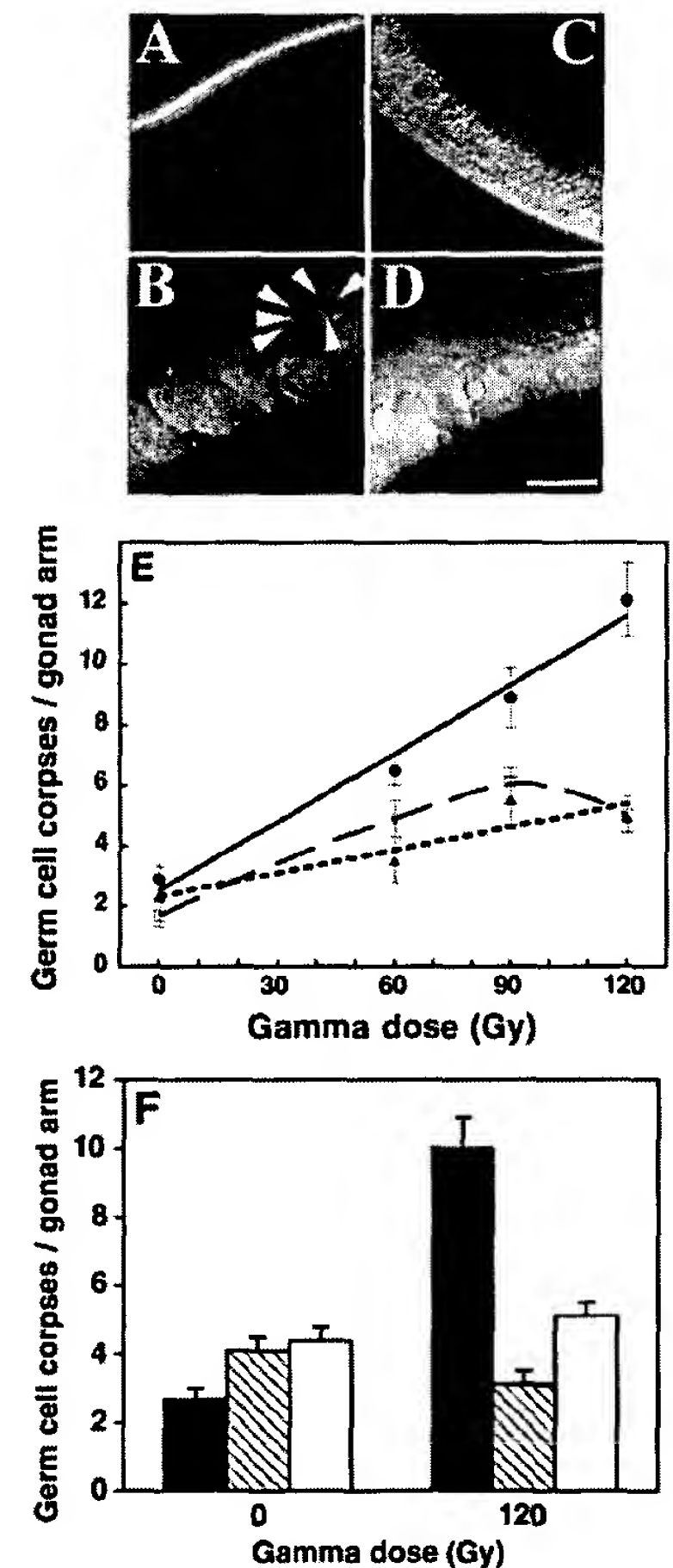
Unlike somatic cells, which have a fixed cell division program, germ-line nuclei in *C.*

*elegans* undergo indeterminate rounds of division and are subject to checkpoint control and apoptosis in response to genotoxic stresses (11); they also undergo developmentally programmed "physiological" cell death, which appears to be regulated by distinct



of Mdm-2 with human p53 (35, 36). The region of highest conservation lies in the DNA binding domain (domains II to V), where several amino acids have been shown to contact the major and minor grooves of the p53 binding site in the DNA-p53 cocrystal (34). These include four of the five most frequently mutated Arg residues in human cancer (asterisks), as well as Cys and His residues (carets) that make critical contacts with DNA in the three-dimensional structure of human p53. The fifth cancer "hot spot" Arg is conservatively substituted with a Lys in CEP-1 (diamond). The CEP-1 sequence corresponds to F52B5.5 reported by the *C. elegans* Sequencing Consortium (GenBank accession number CAA99857).

**Fig. 1.** Conservation of transactivation and DNA binding domains in *C. elegans* CEP-1. (A) Low-resolution three-dimensional model of CEP-1 DNA binding domain (residues 22 to 197) created with the program Modeler/Insight II 98.0 (33). The coordinates of residues 108 to 298 from the crystal structure of the human p53 DNA binding domain were used as the template (34). Conserved Arg residues that make contact with the consensus DNA binding site and that are the most frequently mutated residues in human cancer are shown in red. Amino acids in yellow represent conserved Cys and His residues that coordinate a Zn ion. Portions of the structure shown in magenta are the  $\beta$  strands of the core domain. The green rod indicates the H2 helix that makes contacts with the DNA. (B) Alignment of conserved domains in p53 family members. Single-letter abbreviations for amino acid residues are as follows: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr. Black boxes indicate amino acids that are identical in at least four of the sequences; gray boxes indicate conservative substitutions. Several residues in the NH<sub>2</sub>-terminal transactivation domain (domain I) are conserved in CEP-1, including Leu<sup>38</sup> and Trp<sup>39</sup>, which are necessary for transcriptional activation and for the physical interaction



**Fig. 2.** Requirement of *cep-1* for normal activation of germ cell apoptosis in response to DNA damage. Shown are wild-type (A and B) and *cep-1(w40)* adults (C and D) observed by differential interference contrast (DIC) microscopy 12 hours after the L4 stage, either without radiation [(A) and (C)] or after exposure to 60-Gy IR [(B) and (D)]. Arrowheads point to germ cell corpses in a single focal plane. (E) Quantification of germ cell corpses with increasing doses of IR in wild-type (—), *cep-1(w40)* (---), and *cep-1(RNAi)* adults (····). (F) Dominance of *cep-1(w40)* allele in suppressing DNA damage-induced germ cell apoptosis. Data are shown for wild type (solid bars), *cep-1(w40)/+* heterozygotes (hatched bars), and *cep-1(w40)* homozygotes (open bars) in the absence versus presence of 120-Gy IR. L4-stage hermaphrodites were irradiated with gamma rays from a <sup>137</sup>Cs source, and after 24 hours the number of apoptotic germ cells per gonad arm was determined in 10 to 15 animals. Error bars are SEM.



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signaling pathways upstream of the core apoptotic machinery (12). DNA damage activates germ cell apoptosis through a conserved checkpoint pathway that includes the *rad-5* and *mrt-2* genes and the gene altered by the *op241* mutation; however, none of these genes is required for physiological germ cell death (11). Because p53 coordinates cellular responses to DNA damage, we hypothesized that *cep-1* might regulate apoptosis in the germ line in response to genotoxic stress. Indeed, *cep-1(w40)* hermaphrodites are resistant to ionizing radiation (IR)-induced apoptosis of germ cells (Fig. 2), and *cep-1(RNAi)* phenocopies this effect of *w40* (Fig. 2E). This block in activation of the germ-line cell death program may be general to DNA damage because *cep-1(w40)* mutants, like *rad-5*, *mrt-2*, and *op241* mutants (11), also fail to undergo germ cell death induced by the DNA modifying compound *N*-ethyl-*N*-nitrosourea (10).

Our observations suggest that the truncated CEP-1(w40) protein interferes with the

proapoptotic activity of wild-type CEP-1. Both a heterozygous *w40* mutation and overexpression of the *cep-1(w40)* gene from a heat shock promoter in a wild-type background confer resistance to IR-induced germ cell apoptosis, confirming that *w40* dominantly attenuates wild-type *cep-1* function (Fig. 2F) (10).

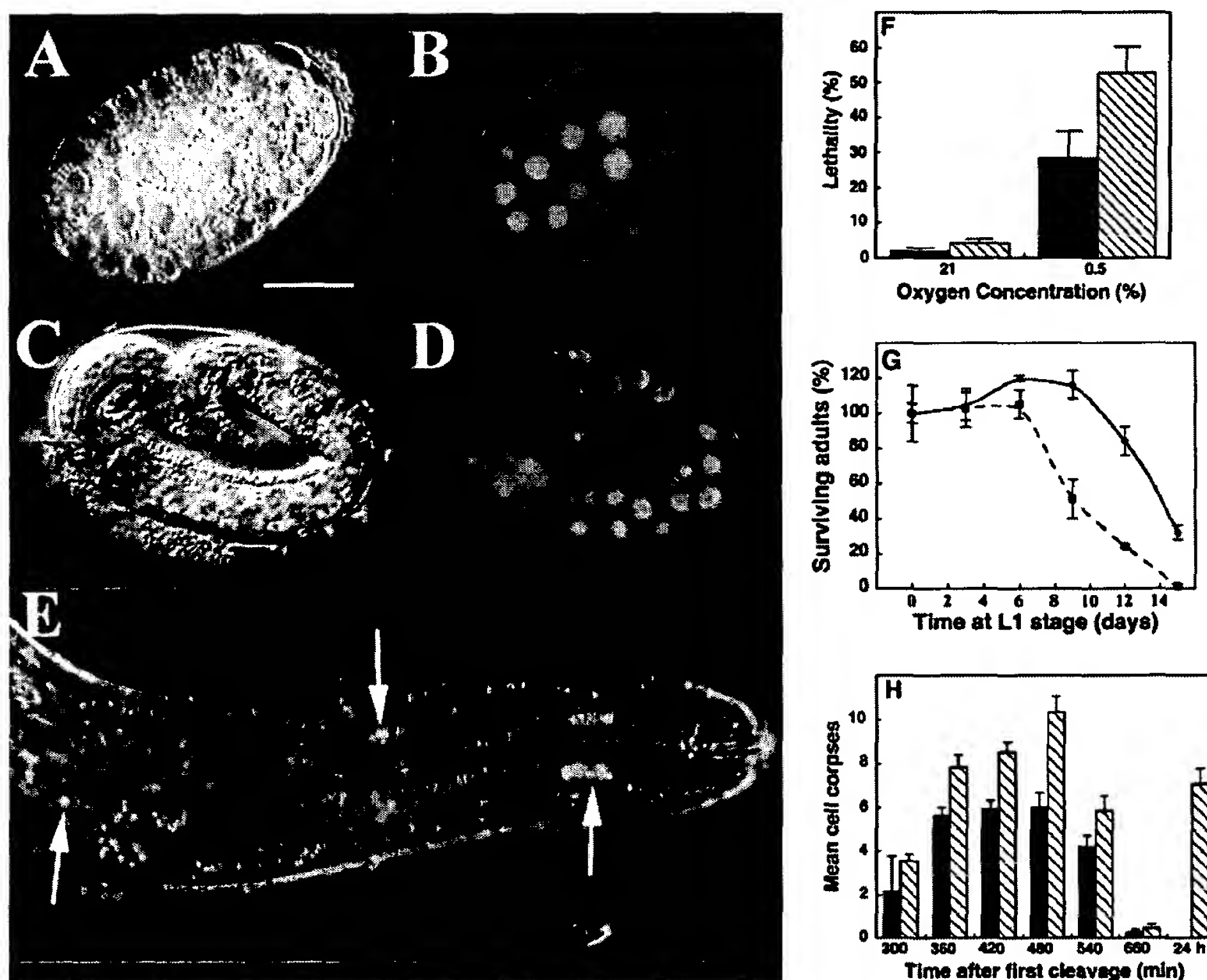
Unlike *rad-5*, *mrt-2*, and *op241* mutants, which are defective in both germ cell apoptosis and cell cycle checkpoint arrest induced by DNA damage, *cep-1(w40)* and *cep-1(RNAi)* germ cells undergo a transient cell cycle arrest in response to IR that is indistinguishable from that of the wild type (10). Furthermore, ectopic expression of CEP-1 in early embryos fails to cause cell division arrest. This ability to activate apoptosis but not arrest the cell cycle is a property shared by *Drosophila* p53, but not vertebrate homologs (3, 4), possibly revealing a primordial role for p53 proteins in apoptosis specifically.

Analysis of animals depleted for *cep-1*

function also uncovered a meiotic role in the absence of genotoxic stress. Nondisjunction of the X chromosome at meiosis I in the hermaphrodite germ line generates nullo-X gametes, leading to XO male progeny (13). We found that depletion of *cep-1* function by RNAi causes an increase in production of males (the Him phenotype, for high incidence of males) under normal growth conditions (Table 1). This effect was observed uniformly among broods of individual hermaphrodites, which implies that *cep-1* is required for chromosome segregation during meiosis rather than during the mitoses preceding meiosis. Mitotic proliferation of nuclei missing an X chromosome would be expected to produce much more variable broods, some with very high numbers of males. The *cep-1(w40)* mutant does not show a Him phenotype, which suggests that the truncated protein does not interfere with the meiotic chromosome segregation activity of CEP-1.

The low frequency of embryonic lethality in *cep-1* mutants (Table 1) might result from

**Fig. 3.** Expression and requirement of *cep-1* in somatic cells. (A to E) Zygotic expression pattern of a CEP-1::GFP fusion reporter in embryos and larvae. Shown are DIC (A and C) and fluorescence (B and D) images of embryos at ~50-cell (A and B) and pretzel (C and D) stages. Similar expression patterns were observed in six independent lines (10). Scale bar, ~10  $\mu$ m. (E) Overlay of GFP and DIC images of CEP-1 expression in pharynx after hatching. Anterior is to the right. Arrows point to nucleolar localization of CEP-1::GFP in anterior m2 muscle cells and other pharyngeal muscle and neurons of an L3-stage hermaphrodite. (F) Lethality of wild-type (solid bars) and *cep-1(w40)* embryos (hatched bars) under normoxic (21% O<sub>2</sub>) and hypoxic (0.5% O<sub>2</sub>) conditions. Early embryos were placed in chambers maintained with a constant atmosphere at the indicated oxygen concentration, as measured with a Systech oxygen analyzer. Lethality (percent  $\pm$  SEM) was scored by quantifying the number of surviving adults arising from a known number of embryos. (G) Effect of prolonged L1 starvation on survival to adulthood of *cep-1(w40)* (■) and wild-type larvae (□). Embryos were collected from gravid adults by hypochlorite treatment and hatched in M9 buffer with cholesterol (10  $\mu$ g/ml) at 20°C in the absence of food. Aliquots of arrested L1 larvae were taken every 72 hours and grown on NGM plates with OP50 bacteria. The fraction surviving to adulthood was determined after 3 days of growth at 20°C. We observed a slight increase in the number of



wild-type surviving adults between 6 and 9 days; this likely reflects sticking of some larvae to the culture tube at earlier time points. (H) Quantification of apoptotic death throughout embryonic stages after overexpression of wild-type CEP-1 (hatched bars) compared with overexpression of CEP-1(w40) (solid bars) by heat shock. Embryos between the 50- and 100-cell stage were collected from gravid adults and heat-shocked at 34°C for 15 min; cell corpses were quantified as the embryos developed. Error bars are SEM.



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autosomal meiotic nondisjunction or could reflect an essential function during normal embryogenesis. Consistent with the latter notion, we found that zygotic expression of a CEP-1::GFP fusion reporter is first detected at the ~50-cell stage and appears to be ubiquitous throughout embryonic development (14) (Fig. 3, A to D). Near the end of embryogenesis, GFP fluorescence decreases; after hatching, expression is restricted to a subset of pharynx cells, becoming concentrated in nucleoli (Fig. 3E).

Although little is known about the role of p53 in embryogenesis, knockout mice have revealed a role in normal development (15). p53 is also highly expressed embryonically in mice and frogs; however, its precise role during embryogenesis remains unclear (16–18). The high levels of ubiquitous CEP-1 expression in *C. elegans* might serve a protective function during embryogenesis, when cell division is rapid and replication errors are likely to occur at a higher frequency. However, *cep-1(w40)* embryos and larvae are not resistant to IR, the intensity and pattern of CEP-1::GFP expression does not change in response to this treatment, and the pattern of apoptosis in *cep-1(w40)* or *cep-1(RNAi)* embryos is indistinguishable from that of the wild type (10). Thus, the proapoptotic function of CEP-1 may be restricted to germ-line cells. Because somatic cells in *C. elegans* cannot generally be replaced if damaged, and arise by a determinate number of cell divisions (and hence are less likely to become tumorous), damage-induced apoptosis in the soma could be detrimental to the animal. In contrast, the germ line contains an excess of germ cells that are not used in self-fertilizing hermaphrodites, and damaged germ cells that are not eliminated could result in defective progeny, making it desirable to eliminate these expendable cells.

Because the DNA damage checkpoint function of CEP-1 is apparently restricted to the germ line, we reasoned that somatic CEP-1 might instead activate a response to other stresses. In vertebrates, p53 is activated by diverse stress signals, including hypoxia,

which leads to stabilization of the protein (19, 20). As a soil-dwelling nematode, *C. elegans* is likely to encounter hypoxic environments frequently. Indeed, we found that *cep-1(w40)* mutants are hypersensitive to the lethal effects of hypoxia (Fig. 3F).

Under conditions of starvation stress, *C. elegans* first-stage (L1) larvae undergo developmental arrest until food is available. We found that the life-span of *cep-1(w40)* larvae is reduced relative to the wild type when they were starved at the L1 stage (Fig. 3G). Wild-type survival was reduced by 50% after ~14 days, whereas survival of *cep-1(w40)* larvae was reduced by the same magnitude after only ~9 days (Fig. 3G). In contrast, we found that the life-span of mutant animals during normal growth was unaffected (10). The effect of starvation- and hypoxia-induced stress on *cep-1* mutants suggests that CEP-1 can modulate responses to both genotoxic stress in the germ line and environmental stress in the soma.

To address the importance of maintaining proper CEP-1 levels during development, we overexpressed CEP-1 from a heat shock-inducible promoter in 50- to 100-cell-stage embryos (21). The resultant embryos often arrested before hatching and showed severe morphological abnormalities. These embryos did not undergo cell cycle arrest, but they showed a significant increase in the number of cell corpses that accumulated throughout embryogenesis; some terminally arrested embryos contained as many as 40 cell corpses (Fig. 3H) at a time when wild-type animals contain virtually none. No apoptotic corpses were observed when CEP-1 was overexpressed in a mutant lacking CED-3 caspase function (10), which is required for all developmentally programmed cell deaths (22). CEP-1-overexpressing embryos that underwent apparently normal development, and that did not show significantly elevated numbers of cell corpses, nevertheless invariably succumbed, arresting before hatching or as L1 larvae with widespread signs of necrosis. Indeed, overexpression of CEP-1 at all larval stages and during adulthood also caused pen-

etrant lethality and widespread necrotic cell death, independent of CED-3 caspase function. All larvae overexpressing the protein became uncoordinated within 8 hours after induction of *cep-1* overexpression and eventually degenerated.

The lethality of overexpressed CEP-1 appears to be a specific effect, as it requires an intact DNA binding domain; overexpression of the truncated *cep-1(w40)* allele resulted in virtually no effect on viability. Moreover, we found that expression of human p53 results in similar degenerative phenotypes in *C. elegans* embryos and larvae (10), which suggests that human p53 and nematode CEP-1 can perform similar biochemical functions. The lethality of overexpressed *cep-1* does not appear to result from activation of the core apoptotic machinery, because mutations in *ced-3* or *ced-4* (22) did not block these effects (10). However, dying animals contained large numbers of nuclei that stained positive for acridine orange, generally regarded as a marker of apoptosis (23). Therefore, high levels of CEP-1 may override the requirement for the CED-3 caspase and activate a caspase-independent cell death program, perhaps analogous to the caspase-independent apoptosis observed recently in other systems, which is revealed when caspase function is blocked in cells otherwise programmed to die (24).

We find that *C. elegans* p53 functions both during normal development (e.g., to ensure proper meiotic chromosome segregation) and under conditions of cellular and genotoxic stress (e.g., in response to DNA damage, hypoxia, or starvation). Although it is expressed ubiquitously in embryos, *cep-1* must be carefully regulated because elevated levels of CEP-1 protein are invariably lethal. It should now be possible to use *C. elegans* as a genetic system to screen for modifiers of the *cep-1* mutant phenotype, allowing a comprehensive dissection of the pathways through which p53-like proteins function to mediate stress response, to activate germ-line apoptosis, and to regulate meiotic chromosome segregation.

**Table 1.** Elimination of *cep-1* function causes meiotic X chromosome nondisjunction.

Genotype	Total F <sub>1</sub> 's	Total dead eggs	Percent dead eggs	Total males*	Percent males
<i>unc-22(RNAi)</i> †	3971	32	0.8	2	0.1
<i>cep-1(RNAi)</i> †	2355	113	4.8	33	1.4
N2‡	2464	2	0.08	4	0.2
<i>cep-1(w40)</i> ‡	3286	38	1.2	10	0.3

\*Males produced by *cep-1(RNAi)* hermaphrodites mated normally and produced the expected frequency of male cross progeny (10), implying that CEP-1 is needed for a function in normal meiotic chromosome segregation and not for sexual identity per se. †Between 15 and 20 L4-stage N2 hermaphrodites were soaked in *cep-1* double-stranded RNA (~5 mg/ml) for 16 to 18 hours at 20°C. Soaked adults were transferred every 24 hours, and dead eggs, males, and hermaphrodites were scored in the F<sub>1</sub> generation. *unc-22(RNAi)* was used as a negative control; although this RNAi treatment invariably results in a penetrant Unc-22 phenotype, no significant effect on male production or viability was seen. ‡N2 (wild-type) and *cep-1(w40)* strains were soaked in M9 buffer for 16 to 18 hours at 20°C and scored as described above.

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7. The amino acid sequence of squid (*Loligo forbesi*) p53 (U43595) was used as a query to search the *C. elegans* database with the PSI-BLAST algorithm (25). Several low-scoring *C. elegans* open reading frames were identified and aligned with several p53 family members using the Block Maker tool (26). F52B5.5 was the only predicted *C. elegans* gene identified with the appropriate p53 signature sequences in the correct modular order. There are seven exons in *cep-1*, and the intron-exon boundaries are in similar positions to those in the murine and human

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- p53* genes (27, 28), underscoring their evolutionary relatedness.
8. We screened 48,000 wild-type (N2) genomes for a *cep-1* deletion using 4,5',8-trimethylpsoralen/ultraviolet light mutagenesis as described (29, 30). First-round polymerase chain reaction primers flanking *cep-1* were 5'-GGTGGACTGTGCTTTGAAATCAAGACTGC-3' and 5'-GCTCTTGATGTTGCCAACAA-GATCGGATTC-3'. Second-round primers were 5'-CAGGGGAGTTGGCGTTAGG-3' and 5'-AATTGGTACAGCGACTTCTCTCA-3'. A single worm containing the *cep-1(w40)* deletion was identified. This deletion removes 1823 nucleotides of the gene, corresponding to nucleotides 28,754 to 31,967 on cosmid F52B5. The splice acceptor and donor sites remain intact in the *cep-1(w40)* allele, which is predicted to encode an in-frame but truncated protein missing amino acids 69 to 242. Further analysis showed that the deletion strain also carries an intact copy of *cep-1*. The *w40* allele segregates independently of the wild-type *cep-1* locus, indicating that the deleted copy had translocated to another region of the genome and a wild-type copy of *cep-1* remains at the normal locus.
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# Integration Between the Epibranchial Placodes and the Hindbrain

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**Developmental integration results from coordination among components of different embryonic fields to realize the later anatomical and functional relationships. We demonstrate that in the chick head, integration between the epibranchial placodes and the hindbrain is achieved as the neuroglial hindbrain crest cells guide the epibranchial neuronal cells inward to establish their central connections. This work defines a role for the neuroglial hindbrain crest in organizing the afferent innervation of the hindbrain.**

After regional specification, during which constituent parts of an embryonic field are defined, the next developmental challenge is that of integration, during which the different embryonic fields are coordinated, and thus, later anatomy and function established. Developmental integration is particularly apparent in the vertebrate head, because head development involves integration of a number of disparate embryonic cell types (1). Here, we studied in the chick the development of the epibranchial ganglia: the geniculate, petrosal, and nodose, which convey gustatory and viscerosensory information from the oro-pharyngeal cavity to central sensory nuclei in the hindbrain (Fig. 1, A and B) (2). The sensory neurons of these ganglia originate in the epibranchial placodes and connect to the central nervous system (CNS) (3, 4). These placodes are focal thickenings of ectoderm close to the tips of the pharyngeal pouches, and which are induced by the pharyngeal endoderm through the action of Bmp-7 (5). It has been unclear, however, how the neuronal cells generated by the epibranchial placodes migrate internally to the site of ganglion formation. We show here that this process is mediated by the neuroglial rhombencephalic neural crest. The epi-

branchial neuronal cells move inward along the tracks of neuroglial neural crest that extend from the hindbrain to the placodes. These results define a role for the neuroglial hindbrain neural crest in the integration of hindbrain and epibranchial placode development.

With a view toward understanding this process, we characterized the migratory paths taken by the epibranchial placodal cells as they move internally. The placodal cells were labeled by application of the lipophilic dye DiI to the exterior of the embryo, at stages concomitant with the induction of these placodes (6). This procedure results in the labeling of the embryonic ectoderm. Cells that leave this tissue layer carry the label with them as they move inward (Fig. 1). Cells migrating from both the geniculate and the petrosal placodes form organized streams extending from the placodal ectoderm toward the hindbrain (Fig. 1).

The migratory paths formed by the epibranchial neuronal cells are reminiscent of those formed by another group of cells, the neural crest. The neural crest cells in this region of the embryo migrate as segregated streams from specific axial levels of the hindbrain (Fig. 2A) (7, 8). The crest cells within these streams, however, have two distinct fates. The early ventrally migrating population fill the underlying pharyngeal arches and form ectomesenchymal derivatives within these structures, whereas the

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